

GenCore version 4.5  
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# OM protein - protein search, using sw model

Run on: January 4, 2002, 18:04:35 ; Search time 38.05 Seconds  
(without alignments)  
208.301 Million cell updates/sec

Title: US-09-875-221a-11

Perfect score: 559

Sequence: 1 DIQMGTSSSLASVGDRTV.....COQNYIPLEFGGKVEIK 107

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

- 1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:\*
- 2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:\*
- 3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:\*
- 4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:\*
- 5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:\*
- 6: /SIDSR/gcgdata/geneseq/geneseq/AA1985.DAT:\*
- 7: /SIDSR/gcgdata/geneseq/geneseq/AA1986.DAT:\*
- 8: /SIDSR/gcgdata/geneseq/geneseq/AA1987.DAT:\*
- 9: /SIDSR/gcgdata/geneseq/geneseq/AA1988.DAT:\*
- 10: /SIDSR/gcgdata/geneseq/geneseq/AA1989.DAT:\*
- 11: /SIDSR/gcgdata/geneseq/geneseq/AA1990.DAT:\*
- 12: /SIDSR/gcgdata/geneseq/geneseq/AA1991.DAT:\*
- 13: /SIDSR/gcgdata/geneseq/geneseq/AA1992.DAT:\*
- 14: /SIDSR/gcgdata/geneseq/geneseq/AA1993.DAT:\*
- 15: /SIDSR/gcgdata/geneseq/geneseq/AA1994.DAT:\*
- 16: /SIDSR/gcgdata/geneseq/geneseq/AA1995.DAT:\*
- 17: /SIDSR/gcgdata/geneseq/geneseq/AA1996.DAT:\*
- 18: /SIDSR/gcgdata/geneseq/geneseq/AA1997.DAT:\*
- 19: /SIDSR/gcgdata/geneseq/geneseq/AA1998.DAT:\*
- 20: /SIDSR/gcgdata/geneseq/geneseq/AA1999.DAT:\*
- 21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	92.7	126	AAW04387	Chimaeric human/mu
2	515	92.1	107	AAV56680	Anti-erythropoietin
3	514	91.9	126	AAV76665	Human/murine chime
4	514	91.9	126	AAW04380	Chimaeric human/mu
5	511	91.4	126	AAV76666	Human/murine chime
6	511	91.4	126	AAW04381	Chimaeric human/mu
7	510	91.2	126	AAV76667	Human/murine chime
8	510	91.2	126	AAW04382	Chimaeric human/mu
9	509	91.1	126	AAV76669	Human/murine chime
10	509	91.1	126	AAV76671	Human/murine chime
11	509	91.1	126	AAW04384	Chimaeric human/mu

12	509	91.1	126	AAW04386	Chimaeric human/mu
13	508	90.9	126	AAV76672	Human/murine chime
14	507	90.7	126	AAV76680	Human/murine chime
15	507	90.7	126	AAV76678	Human/murine chime
16	507	90.7	126	AAW04383	Chimaeric human/mu
17	507	90.7	126	AAW04393	Chimaeric human/mu
18	507	90.7	126	AAW04395	Chimaeric human/mu
19	507	90.7	126	AAV76682	Human/murine chime
20	507	90.7	126	AAW04397	Chimaeric human/mu
21	505	90.3	126	AAV76670	Human/murine chime
22	505	90.3	126	AAW04385	Chimaeric human/mu
23	503	90.0	126	AAV76675	Human/murine chime
24	503	90.0	126	AAW04390	Chimaeric human/mu
25	502.5	89.9	109	AAV65164	Humanised anti-PR1
26	502	89.8	107	AAV62085	Humanised Fab vers
27	502	89.8	107	AAV60338	Humanised anti-Erb
28	502	89.8	107	AAV61583	Humanised Fab vers
29	500	89.4	126	AAV76679	Human/murine chime
30	500	89.4	126	AAW04394	Chimaeric human/mu
31	499	89.3	126	AAV76668	Human/murine chime
32	495	88.6	126	AAV76673	Human/murine chime
33	495	88.6	126	AAW04388	Chimaeric human/mu
34	495	88.6	126	AAW04391	Chimaeric human/mu
35	492	88.0	102	AAV56683	Humanized 3G9 11qB
36	492	88.0	108	AAV19749	Erythropoietin rec
37	490	87.7	126	AAV76676	Human/murine chime
38	489	87.5	126	AAV76674	Human/murine chime
39	489	87.5	126	AAW04389	Chimaeric human/mu
40	488	87.3	108	AAV19751	Erythropoietin rec
41	486	86.9	108	AAV19752	Erythropoietin rec
42	486	86.9	237	AAV24047	light chain of 4D5
43	486	86.9	252	AAV28158	Human anti-c-ErbB2
44	486	86.9	698	AAV83453	4D5 Fab molecule e
45	485	86.8	126	AAV43691	PBI.3/Humanised 11

## ALIGNMENTS

RESULT	1
AAW04387	
ID	AAW04387 standard; Protein; 126 AA.
AC	AAW04387;
DT	09-DEC-1996 (first entry)
DE	Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21h-g(kappa)
XX	
XX	Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW	chimaera; single stranded Fv region; low human antigenicity;
KW	diagnosis; treatment; cerebral tumour; reshaped.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Peptide
FT	Peptide
FT	Peptide
FT	Region
FT	Region
FT	Region
FT	Region
PN	JP08169900-A.
XX	
PD	02-JUL-1996.
XX	
PF	18-NOV-1994; 94JP-0285057.
XX	

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PR 18-OCT-1994; 94UP-0252166.
PR 19-NOV-1993; 93UP-0291078.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX
XX WPI: 1996-358509/36.
XX N-PSDB; AAT38628.
XX
XX Reshaped anti-human myeloblastoma cell human antibody - has low
XX human antigenicity, and is therefore useful for diagnosis and
XX treatment of cerebral tumours, e.g. myeloblastoma
XX
XX Example 5; Page 30; 45pp; Japanese.
XX
XX The present sequence is a fragment of the chimaeric human/murine
XX monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by
XX combining light and heavy variable region DNA, from a murine
XX anti-human myeloblastoma cell MAb, with human light and heavy
XX constant region sequences, respectively to produce chimaeric
XX human/murine light and heavy chain DNA mols.. A recombinant vector
XX for the expression of the heavy and light chain DNA mols. was
XX prepd., and used to transform a host cell. The host cell was then
XX cultured, and the expression prods. of the heavy and light chain
XX DNA mols. sepd. and connected with a peptide linker to produce a
XX single stranded Fv region. The reshaped Fv region has low human
XX antigenicity, and is therefore expected to be useful as an agent
XX for the diagnosis and treatment of cerebral tumours,
XX e.g. myeloblastoma.
XX
XX Sequence 126 AA:
SQ
Query Match 92.7%; Score 518; DB 17; Length 126;
Best Local Similarity 93.5%; Pred. No. 4.3e-31;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTWAWYQOKPKGAPRLIYASFLYSGVPY 60
DB 20 dIqmtqspsslsasvgrvtitckasqnvgtwawyqkpkapRLIYsasyrsgvps 79
QY 61 RFGSGSGTDFLTITSSLOPEFATYVCOQVNIYPLTFGCGTKVEIK 107
DB 80 rfgsgsgtdfltltslqpediatycqynsyprafggtkveik 126
RESULT 2
AAV56680
ID AAV56680 standard; protein: 107 AA.
XX
XX AAV56680;
XX
XX 15-FEB-2000 (first entry)
XX
XX Anti-erythropoietin receptor MAb 3G9 light chain variable region.
XX
XX Complementarity determining region; antibody; primate; immunogenicity;
XX Old World ape; Old World monkey; antigen-binding affinity.
XX
XX Synthetic.
XX Mus sp.
XX Pan troglodytes.
XX
XX MO9953369-A1.
XX
XX 04-NOV-1999.
XX
XX 28-APR-1999; 99WO-US09131.
XX
XX 28-APR-1998; 98US-0083367.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Taylor AH;
PI
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XX
XX WPI: 2000-023265/02.
XX
XX Antibodies containing donor complementarity determining regions and
XX non-human primate acceptor frameworks, having reduced immunogenicity in
XX humans -
XX
XX Example 8; Page 114-115; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
XX (complementarity determining regions) derived from a non-human antigen-
XX specific donor antibody, and an acceptor framework from a non-human
XX primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX specific donor antibody onto homologous Old World ape or monkey acceptor
XX frameworks. The Abs have reduced immunogenicity and are better tolerated
XX in humans (because of the close similarity between the human and primate
XX proteins), but retain the full antigen-binding affinity of the donor
XX antibody.
XX
XX Sequence 107 AA:
SQ
Query Match 92.1%; Score 515; DB 21; Length 107;
Best Local Similarity 93.5%; Pred. No. 6.2e-31;
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTWAWYQOKPKGAPRLIYASFLYSGVPY 60
DB 1 dIqmtqspsslsasvgrvtitckasqnvgtwawyqkpkapRLIYsasyrsgvps 60
QY 61 RFGSGSGTDFLTITSSLOPEFATYVCOQVNIYPLTFGCGTKVEIK 107
DB 61 rfgsgsgtdfltltslqpediatycqynsypltfggtkveik 107
RESULT 3
AAV76665
ID AAV76665 standard; protein: 126 AA.
XX
XX AAV76665;
XX
XX 17-JAN-1996 (first entry)
XX
XX Human/murine chimeric antibody HEF-RVL-M21a-g kappa.
XX
XX Human; murine; chimeric antibody; HEF-RVL-M21a-g kappa;
XX medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..19
XX FT Peptide /label= sig-peptide
XX FT Peptide 20..43
XX FT /label= FR 1
XX FT Peptide 44..54
XX FT /label= CDR 1
XX FT Peptide 55..69
XX FT /label= FR 2
XX FT Peptide 70..76
XX FT /label= CDR 2
XX FT Peptide 77..108
XX FT /label= FR 3
XX FT Peptide 109..117
XX FT /label= CDR 3
XX FT Peptide 118..126
XX FT /label= FR 4
XX
XX MO9514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX
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xx	19-NOV-1993:	93JP-0291078.	
xx	(CHUS )	CHUGAI SEIYAKU KK.	
xx	Ohlomo T, Sato K, Tsuchiya M;		
xx	WPI: 1995-200347/26.		
xx	N-PSDB; AAO94499.		
xx	Reconstituted antibody against human medullo- blastoma cells - contains high proportion of human antibody origin and has low antigenicity		
xx	Claim 33; Page 64; 120pp; Japanese.		
xx	AAO94499 encodes AAR76665 the human/murine chimeric antibody HEF- RVL-M21a-g kappa. The antibody is reactive with human medullo- blastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.		
xx	Sequence 126 AA;		
xx	Query Match	91.9%; Score 514; DB 16; Length 126;	
xx	Best Local Similarity	92.5%; Pred. No. 8,4e-31;	
xx	Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;		
Oy	1 DIOMQSPSSLASASGDRRTTTCRKASONGTVNAVYQOKPGKAPKLLIYSASFLYSGVPY 60		
Db	20 dIQMTQSPSSLSASygdvrltclckasqngvltvayyqdkpypakpLLIYsaayrYsgvps 79		
Oy	61 RFGSGSGCTDFTLLTISLQPEDFATVYCOQNYIPLTFSGQTKVEIK 107		
Db	80 rfgsgsgldftfltslqpediatlyycqynsyprafgqtkvEik 126		
RESULT 4			
AAW04380			
ID	AAW04380 standard; Protein: 126 AA.		
xx	AAW04380;		
xx	09-DEC-1996 (first entry)		
DE	Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21a-g(kappa).		
xx	Murine; human; myeloblastoma; chimaera; monoclonal antibody;		
KW	chimaera; single stranded Fv region; low human antigenicity;		
xx	diagnosis; treatment; cerebral tumour; reshaped.		
xx	Synthetic.		
xx	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT	Peptide	/label= sig_peptide	
FT	Peptide	20..125	
FT	Peptide	/label= mat_peptide	
FT	Region	33..53	
FT	Region	/label= CDR_1	
FT	Region	69..75	
FT	Region	/label= CDR_2	
FT	Region	108..116	
FT	Region	/label= CDR_3	
xx	JP08169900-A.		
xx	02-JUL-1996.		
xx	18-NOV-1994;	94JP-0285057.	
xx	18-OCT-1994;	94JP-0252166.	
xx	19-NOV-1993;	93JP-0291078.	

[illegible]

FT	Peptide	118..126
FT		/label= FR 4
XX		
PN	W09514041-A1.	
XX		
PD	26-MAY-1995.	
XX		
PF	19-OCT-1994;	94WO-JP01763.
XX		
PR	19-NOV-1993;	93JP-0291078.
XX		
PA	(CHUS ) CHUGAI SEIYAKU KK.	
XX		
PI	Ohtomo T, Sato K, Tsuchiya M;	
XX		
DR	WPI; 1995-200347/26.	
XX		
PT	Reconstituted antibody against human medullo:blastoma cells -	
PT	contains high proportion of human antibody origin and has low	
PT	antigenicity	
XX		
PS	Claim 33; Page 66; 120pp; Japanese.	
XX		
CC	AA094502 encodes AAR76666 the human/murine chimeric antibody HEF-	
CC	RV-M21b-g-kappa. The antibody is reactive with human medullo-	
CC	blastoma (a brain tumour) cells. The chimeric antibody can be	
CC	used in the diagnosis and treatment of this disease.	
XX		
S0	Sequence 126 AA;	
	Query Match	91.4%; Score 511; DB 16; Length 126;
	Best Local Similarity	91.6%; Pred. No. 1,4e-30;
	Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps	0;
OY	1 DIOMQSPSSLSASVGDRTITCRASONVGTWAWYQOKPKGAPKILLYSASFLYSGVPY 60	
DB	20 diqmtqspsslsasvqdvrtltckasqngvawyqdkpkpapklllysasrysyvps 79	
OY	61 RFGSGSGTDFLTRITRISLOPEDFATRYCOQYNIYPLTREGQTKVEIK 107	
DB	80 rfsgsgsgtdyftltslqpediatrycqynsyprafgqgkveik 126	
	RESULT 6	
	AAW04381	
ID	AAW04381 standard; Protein; 126 AA.	
XX		
AC	AAW04381;	
XX		
DT	09-DEC-1996 (first entry)	
XX		
DE	Chimaeric human/murine MAB ONS-M21 fragment HEF-RVL-M21b-g(kappa).	
XX		
KW	Murine; human; myeloblastoma; chimaera; monoclonal antibody;	
KW	chimaera; single stranded Fv region; low human antigenicity;	
KW	diagnosis; treatment; cerebral tumour; reshaped.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= sig_peptide
FT	Peptide	20..125
FT		/label= mat_peptide
FT	Region	33..53
FT		/label= CDR_1
FT	Region	69..75
FT		/label= CDR_2
FT	Region	108..116
FT		/label= CDR_3
XX		
XX		
XX	JP08169900-A	

[illegible]



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FT      /label= FR 2
FT      Peptide      70..76
FT      /label= CDR_2
FT      Peptide      77..108
FT      /label= FR_3
FT      Peptide      109..117
FT      /label= CDR 3
FT      Peptide      118..126
FT      /label= FR 4
XX
XX      WO9514041-A1.
XX
XX      26-MAY-1995.
XX
XX      19-OCT-1994; 94MO-JP01763.
XX
XX      19-NOV-1993; 93JP-0291078.
XX
XX      (CHUS ) CHUGAI SEIYAKU KK.
XX
XX      Ohtomo T, Sato K, Tsuchiya M;
XX
XX      WPI; 1995-200347/26.
XX      N-PSDB; AA094505.
XX
XX      Reconstituted antibody against human medulloblastoma cells -
XX      contains high proportion of human antibody origin and has low
XX      antigenicity
XX
XX      Claim 33; Page 68; 120pp; Japanese.
XX
XX      AA094505 encodes AAR76667 the human/murine chimeric antibody HEF-
XX      RVL-M21c-g kappa. The antibody is reactive with human medullo-
XX      blastoma (a brain tumour) cells. The chimeric antibody can be
XX      used in the diagnosis and treatment of this disease.
XX
XX      Sequence 126 AA;

Query Match      91.2%; Score 510; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.6e-30;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 DIQMTQSSSLASVGVDRVTITTKASQNVGNVAMVQOKPKAPKRLIYSASFYSGVPY 60
      |||
      20 diqmtqssslasvsgdrvtitckasqnvgnvawyqkpkp9kpk11lyssasyrsgvps 79

QY      61 RFSGSGSGTDFTLTISSLOPEDFATYYCOQYNIVPLTFGOGTKVEIK 107
      |||
      80 rfsgsgsgtdftltisslqpediatyfcqgynsyprafgqtkveik 126

Db

RESULT      8
AA04382
ID      AA04382 standard; Protein; 126 AA.
XX
XX      AA04382;
XX
XX      09-DEC-1996 (first entry)
XX
XX      Chimeric human/murine Mab ONS-M21 fragment HEF-RVL-M21c-g(kappa).
XX
XX      Murine; human; myeloblastoma; chimera; monoclonal antibody;
XX      chimera; single stranded Fv region; low human antigenicity;
XX      diagnosis; treatment; cerebral tumour; reshaped.
XX
XX      Synthetic.
XX
XX      key      Location/Qualifiers
XX      Peptide      1..19
XX      /label= sig_peptide
XX      Peptide      20..125
XX      /label= mat_peptide
XX

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FT      Region      33..53
FT      /label= CDR_1
FT      Region      69..75
FT      /label= CDR_2
FT      Region      108..116
FT      /label= CDR_3
XX
XX      JP08169900-A.
XX
XX      02-JUL-1996.
XX
XX      18-NOV-1994; 94JP-0285057.
XX
XX      18-OCT-1994; 94JP-0252166.
XX      19-NOV-1993; 93JP-0291078.
XX
XX      (CHUS ) CHUGAI PHARM CO LTD.
XX
XX      WPI; 1996-358509/36.
XX      N-PSDB; AAT38619.
XX
XX      Reshaped anti-human myeloblastoma cell human antibody - has low
XX      human antigenicity, and is therefore useful for diagnosis and
XX      treatment of cerebral tumours, e.g. myeloblastoma
XX
XX      Example 5; Page 26; 45pp; Japanese.
XX
XX      The present sequence is a fragment of the chimeric human/murine
XX      monoclonal antibody (Mab) ONS-M21. The Mab was prepd. by
XX      combining light and heavy variable region DNA, from a murine
XX      anti-human myeloblastoma cell Mab, with human light and heavy
XX      constant region sequences, respectively to produce chimeric
XX      human/murine light and heavy chain DNA mols.. A recombinant vector
XX      for the expression of the heavy and light chain DNA mols. was
XX      prepd., and used to transform a host cell. The host cell was then
XX      cultured, and the expression prods. of the heavy and light chain
XX      DNA mols. sepd. and connected with a peptide linker to produce a
XX      single stranded Fv region. The reshaped Fv region has low human
XX      antigenicity, and is therefore expected to be useful as an agent
XX      for the diagnosis and treatment of cerebral tumours,
XX      e.g. myeloblastoma.
XX
XX      Sequence 126 AA;

Query Match      91.2%; Score 510; DB 17; Length 126;
Best Local Similarity 91.6%; Pred. No. 1.6e-30;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 DIQMTQSSSLASVGVDRVTITTKASQNVGNVAMVQOKPKAPKRLIYSASFYSGVPY 60
      |||
      20 diqmtqssslasvsgdrvtitckasqnvgnvawyqkpkp9kpk11lyssasyrsgvps 79

QY      61 RFSGSGSGTDFTLTISSLOPEDFATYYCOQYNIVPLTFGOGTKVEIK 107
      |||
      80 rfsgsgsgtdftltisslqpediatyfcqgynsyprafgqtkveik 126

Db

RESULT      9
AAR76669
ID      AAR76669 standard; Protein; 126 AA.
XX
XX      AAR76669;
XX
XX      17-JAN-1996 (first entry)
XX
XX      Human/murine chimeric antibody HEF-RVL-M21c-g kappa.
XX
XX      Human; murine; chimeric antibody; HEF-RVL-M21c-g kappa;
XX      medulloblastoma; brain tumour; treatment; diagnosis.
XX
XX      Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= sig_peptide
FT Peptide 20..43
FT Peptide /label= FR 1
FT Peptide 44..54
FT Peptide /label= CDR 1
FT Peptide 55..69
FT Peptide /label= FR 2
FT Peptide 70..76
FT Peptide /label= CDR 2
FT Peptide 77..108
FT Peptide /label= FR 3
FT Peptide 109..117
FT Peptide /label= CDR 3
FT Peptide 118..126
FT Peptide /label= FR 4
XX
XX W09514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ohtomo T, Sato K, Tsuchiya M;
XX
XX WPI: 1995-200347/26.
XX
XX N-PSDB: AA094509.
XX
XX Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
XX Claim 33; Pages 71-72; 120pp; Japanese.
XX
XX AA094509 encodes AAR76669 the human/murine chimeric antibody HEF-
XX CC RVL-M21e-g kappa. The antibody is reactive with human medullo-
XX CC blastoma (a brain tumour) cells. The chimeric antibody can be
XX CC used in the diagnosis and treatment of this disease.
XX
XX SQ Sequence 126 AA:

Query Match 91.1%; Score 509; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 1.9e-30;
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITCKASQNVGTWAWYQOKPGKAPKLLIYSASFYSGVPY 60
DB 20 dIQMTQSPSSLSASVGDRTITCKASQNVGTWAWYQOKPGKAPKLLIYSASFYSGVPY 79
QY 61 RFSGSGSGTDFTLTSSLPEDFATYYCOQYNIYPLTGGGKVEIK 107
DB 80 rfsGSGSGtdftLTlsslpEdfAtYyCqQYnIyPlTgGgKvEiK 126

RESULT 10
AAR76671 ID AAR76671 standard; Protein: 126 AA.
XX
XX AAR76671:
XX
XX 17-JAN-1996 (first entry)
XX
XX Human/murine chimeric antibody HEF-RVL-M21g-g kappa.
XX
XX Human: murine; chimeric antibody; HEF-RVL-M21g-g kappa;
XX
XX medullo:blastoma; brain tumour; treatment; diagnosis.
XX
```

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..19
FH Peptide /label= sig_peptide
FH Peptide 20..43
FH Peptide /label= FR 1
FH Peptide 44..54
FH Peptide /label= CDR 1
FH Peptide 55..69
FH Peptide /label= FR 2
FH Peptide 70..76
FH Peptide /label= CDR 2
FH Peptide 77..108
FH Peptide /label= FR 3
FH Peptide 109..117
FH Peptide /label= CDR 3
FH Peptide 118..126
FH Peptide /label= FR 4
XX
XX W09514041-A1.
XX
XX 26-MAY-1995.
XX
XX 19-OCT-1994; 94WO-JP01763.
XX
XX 19-NOV-1993; 93JP-0291078.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ohtomo T, Sato K, Tsuchiya M;
XX
XX WPI: 1995-200347/26.
XX
XX N-PSDB: AA094513.
XX
XX Reconstituted antibody against human medullo:blastoma cells -
XX contains high proportion of human antibody origin and has low
XX antigenicity
XX
XX Claim 33; Page 75; 120pp; Japanese.
XX
XX AA094513 encodes AAR76671 the human/murine chimeric antibody HEF-
XX CC RVL-M21g-g kappa. The antibody is reactive with human medullo-
XX CC blastoma (a brain tumour) cells. The chimeric antibody can be
XX CC used in the diagnosis and treatment of this disease.
XX
XX SQ Sequence 126 AA:

Query Match 91.1%; Score 509; DB 16; Length 126;
Best Local Similarity 90.7%; Pred. No. 1.9e-30;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTITCKASQNVGTWAWYQOKPGKAPKLLIYSASFYSGVPY 60
DB 20 dIQMTQSPSSLSASVGDRTITCKASQNVGTWAWYQOKPGKAPKLLIYSASFYSGVPY 79
QY 61 RFSGSGSGTDFTLTSSLPEDFATYYCOQYNIYPLTGGGKVEIK 107
DB 80 rfsGSGSGtdftLTlsslpEdfAtYyCqQYnIyPlTgGgKvEiK 126

RESULT 11
AAW04384 ID AAW04384 standard; Protein: 126 AA.
XX
XX AAW04384:
XX
XX 09-DEC-1996 (first entry)
XX
XX Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21e-g(kappa).
XX
XX Murine: human; myeloblastoma; chimaera; monoclonal antibody;
XX
```

KW chimera; single stranded Fv region; low human antigenicity;  
XX diagnosis; treatment; cerebral tumour; reshaped.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= sig-peptide  
FT Peptide 20..125  
FT /label= mat-peptide  
FT Region 33..53  
FT /label= CDR\_1  
FT Region 69..75  
FT /label= CDR\_2  
FT Region 108..116  
FT /label= CDR\_3  
PN JP08169900-A.  
PD 02-JUL-1996.  
XX 18-NOV-1994; 94JP-0285057.  
XX 18-OCT-1994; 94JP-0252166.  
PR 19-NOV-1993; 93JP-0291078.  
XX (CHUS ) CHUGAI PHARM CO LTD.  
XX WPI: 1996-358509/36.  
DR N-PSDB; AAT38623.  
XX Reshaped anti-human myeloblastoma cell human antibody - has low  
PT human antigenicity, and is therefore useful for diagnosis and  
PT treatment of cerebral tumours, e.g. myeloblastoma  
XX Example 5; Pages 27-28; 45pp; Japanese.  
XX The present sequence is a fragment of the chimaeric human/murine  
CC monoclonal antibody (MAb) ONS-M21. The MAb was prep'd. by  
CC combining light and heavy variable region DNA, from a murine  
CC anti-human myeloblastoma cell MAb, with human light and heavy  
CC constant region sequences, respectively to produce chimaeric  
CC human/murine light and heavy chain DNA mols.. A recombinant vector  
CC for the expression of the heavy and light chain DNA mols. was  
CC prep'd., and used to transform a host cell. The host cell was then  
CC cultured, and the expression prods. of the heavy and light chain  
CC DNA mols. sep'd. and connected with a peptide linker to produce a  
CC single stranded Fv region. The reshaped Fv region has low human  
CC antigenicity, and is therefore expected to be useful as an agent  
CC for the diagnosis and treatment of cerebral tumours,  
CC e.g. myeloblastoma.  
XX  
XX Sequence 126 AA:  
SQ  
Query Match 91.1%; Score 509; DB 17; Length 126;  
Best Local Similarity 90.7%; Pred. No. 1.9e-30;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 1 DIQTGSPSSLSASVGDVITCKASQNVGTNAVWYQKPGKAPKLLIYSASFYSGVPY 60  
DB 20 diqmtgspsslsasvgtvsvtkasqngvtnvawyqkpgkpklllysasfysgvs 79  
QY 61 RFSGSGGTFTLTLSLQPEDFATYYCOQYNYPLTFGGGTKEIK 107  
DB 80 rfsgsggtftltlsslqpediatyfcqgynsyprafggtkveik 126  
RESULT 12  
AAW04386  
ID AAW04386 standard; Protein; 126 AA.  
XX  
AC AAW04386;

XX 09-DEC-1996 (first entry)  
DT  
XX  
DE Chimaeric human/murine MAb ONS-M21 fragment HFE-RVL-M21g-g(kappa).  
XX  
XX Murine; human; myeloblastoma; chimera; monoclonal antibody;  
KW chimera; single stranded Fv region; low human antigenicity;  
KW diagnosis; treatment; cerebral tumour; reshaped.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= sig-peptide  
FT Peptide 20..125  
FT /label= mat-peptide  
FT Region 33..53  
FT /label= CDR\_1  
FT Region 69..75  
FT /label= CDR\_2  
FT Region 108..116  
FT /label= CDR\_3  
PN JP08169900-A.  
PD 02-JUL-1996.  
XX 18-NOV-1994; 94JP-0285057.  
XX 18-OCT-1994; 94JP-0252166.  
PR 19-NOV-1993; 93JP-0291078.  
XX (CHUS ) CHUGAI PHARM CO LTD.  
XX WPI: 1996-358509/36.  
DR N-PSDB; AAT38627.  
XX Reshaped anti-human myeloblastoma cell human antibody - has low  
PT human antigenicity, and is therefore useful for diagnosis and  
PT treatment of cerebral tumours, e.g. myeloblastoma  
XX Example 5; Pages 29-30; 45pp; Japanese.  
XX The present sequence is a fragment of the chimaeric human/murine  
CC monoclonal antibody (MAb) ONS-M21. The MAb was prep'd. by  
CC combining light and heavy variable region DNA, from a murine  
CC anti-human myeloblastoma cell MAb, with human light and heavy  
CC constant region sequences, respectively to produce chimaeric  
CC human/murine light and heavy chain DNA mols.. A recombinant vector  
CC for the expression of the heavy and light chain DNA mols. was  
CC prep'd., and used to transform a host cell. The host cell was then  
CC cultured, and the expression prods. of the heavy and light chain  
CC DNA mols. sep'd. and connected with a peptide linker to produce a  
CC single stranded Fv region. The reshaped Fv region has low human  
CC antigenicity, and is therefore expected to be useful as an agent  
CC for the diagnosis and treatment of cerebral tumours,  
CC e.g. myeloblastoma.  
XX  
XX Sequence 126 AA:  
SQ  
Query Match 91.1%; Score 509; DB 17; Length 126;  
Best Local Similarity 90.7%; Pred. No. 1.9e-30;  
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 1 DIQTGSPSSLSASVGDVITCKASQNVGTNAVWYQKPGKAPKLLIYSASFYSGVPY 60  
DB 20 diqmtgspsslsasvgtvsvtkasqngvtnvawyqkpgkpklllysasfysgvs 79  
QY 61 RFSGSGGTFTLTLSLQPEDFATYYCOQYNYPLTFGGGTKEIK 107  
DB 80 rfsgsggtftltlsslqpediatyfcqgynsyprafggtkveik 126

RESULT	13
AAR76672	ID AAR76672 standard; Protein: 126 AA.
XX	
AC	
XX	AAR76672;
DY	17-JAN-1996 (first entry)
XX	
DE	Human/murine chimeric antibody HEF-RVL-M21h-g kappa.
XX	
KW	Human; murine; chimeric antibody; HEF-RVL-M21h-g kappa; medulloblastoma; brain tumour; treatment; diagnosis.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..19
FT	/label= sig_peptide
FT	20..43
FT	Peptide /label= FR 1
FT	44..54
FT	Peptide /label= CDR 1
FT	55..69
FT	/label= FR 2
FT	70..76
FT	Peptide /label= CDR 2
FT	77..108
FT	/label= FR 3
FT	109..117
FT	Peptide /label= CDR 3
FT	118..126
FT	Peptide /label= FR 4
XX	
PN	WO9514041-A1.
XX	
PD	26-MAY-1995.
XX	
PE	19-OCT-1994; 94WO-JP01763.
XX	
PR	19-NOV-1993; 93JP-0291078.
XX	
PA	(CHUS ) CHUGAI SEIYAKU KK.
XX	
PI	Ohtomo T, Sato K, Tsuchiya M;
XX	
DR	WPt: 1995-200347/26.
DR	N-PsDB: AAO94514.
XX	
PT	Reconstituted antibody against human medulloblastoma cells - contains high proportion of human antibody origin and has low antigenicity
XX	
PS	Claim 33; Pages 76-77; 120pp; Japanese.
XX	
CC	AAO94514 encodes AAR76672 the human/murine chimeric antibody HEF-
CC	RVL-M21h-g kappa. The antibody is reactive with human medullo-
CC	blastoma (a brain tumour) cells. The chimeric antibody can be
CC	used in the diagnosis and treatment of this disease.
XX	
SQ	Sequence 126 AA:
Query Match	90.9%; Score 508; DB 16; Length 126;
Best Local Similarity	91.6%; Pred. No. 2.3e-30;
Matches 98; Conservative	2; Mismatches 7; Indels 0; Gaps 0;
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Db	20 dltmgtqssslasavgdvrlctckcasqngvtwavygdkpgkpklllysaayrysgyps 79
YY	61 RFSGSGGTDFTLTISSLQPEDFAITYCOQNYIPLTFGGTKVEIK 107

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Db      80  rftgsqsgcdflltllsslqpediaelyyqgqynsyprateggctkveik 126

RESULT 14
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XX      AAR76680 standard; Protein: 126 AA.
AC      AAR76680;
DT      17-JAN-1996 (first entry)
XX      Human/murine chimeric antibody HEF-RVL-M21p-g kappa.
DE      Human; murine; chimeric antibody; HEF-RVL-M21p-g kappa;
KW      medulloblastoma; brain tumour; treatment; diagnosis.
XX      Homo sapiens.
OS
XX
XX      Key Location/Qualifiers
FH      Peptide 1..19
FT      /label= sig-peptide
FT      Peptide 20..43
FT      /label= FR 1
FT      Peptide 44..54
FT      /label= CDR 1
FT      Peptide 55..69
FT      /label= FR 2
FT      Peptide 70..76
FT      /label= CDR 2
FT      Peptide 77..108
FT      /label= FR 3
FT      Peptide 109..117
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FT      Peptide 118..126
FT      /label= FR 4
XX
XX      WO9514041-A1.
XX
XX      PD 26-MAY-1995.
XX
XX      PF 19-OCT-1994; 94WO-JP01763.
XX
XX      PR 19-NOV-1993; 93JP-0291078.
XX
XX      PA (CHUS ) CHUGAI SEIYAKU KK.
XX
XX      PI Ohtomo T, Sato K, Tsuchiya M;
XX
XX      WI 1, 1995-200347/26.
XX      DR N-PSDB; AAQ94532.
XX
XX      PT Reconstituted antibody against human medullo:blastoma cells -
XX      contains high proportion of human antibody origin and has low
XX      antigenicity
XX
XX      PS Claim 24; Pages 90-91; 120pp; Japanese.
XX
XX      CC AAQ94532 encodes AAR76680 the human/murine chimeric antibody HEF-
XX      RVL-M21p-g kappa. The antibody is reactive with human medullo-
XX      blastoma (a brain tumour) cells. The chimeric antibody can be
XX      used in the diagnosis and treatment of this disease.
XX
XX      SQ Sequence 126 AA;

Query Match 90.7%; Score 507; DB 16; Length 126;
Best Local Similarity 91.6%; Pred. No. 2,7e-30;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY      1 DIQMQRSSSLASASGDRVITITCKRSQNGVGNVAVYQOKPKGKAPKLLLYSASFLYSGVPY 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
20 diqmqrssslsasvsgdrvcltckasqngvgnvavayqkpkpkpillysasvrysgvps 79

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OY 61 RFGSGSGTDFTLTISLQPEDFATYCCOYNIYPLTFGGGTKEIK 107  
 |||||  
 DB 80 rfsqsgsgtdftltisslqpediatyccqynsyprafgqtkveik 126

RESULT 15

AAR76678  
 ID AAR76678 standard: Protein: 126 AA.

AC AAR76678;

DT 17-JAN-1996 (first entry)

DE Human/murine chimeric antibody HEF-RVL-M21n-g kappa.

KW Human; murine; chimeric antibody; HEF-RVL-M21n-g kappa;  
 medulloblastoma; brain tumour; treatment; diagnosis.

OS Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..19 /label= sig\_peptide

FT Peptide 20..43 /label= FR 1

FT Peptide 44..54 /label= CDR 1

FT Peptide 55..69 /label= FR 2

FT Peptide 70..76 /label= CDR 2

FT Peptide 77..108 /label= FR 3

FT Peptide 109..117 /label= CDR 3

FT Peptide 118..126 /label= FR 4

FT Peptide

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DB 20 diqmtqspssiasevgdrvtltckasqnvgnvawyqkpkp9qspk11lysasyrysgvpt 79  
 OY 61 RFGSGSGTDFTLTISLQPEDFATYCCOYNIYPLTFGGGTKEIK 107  
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 DB 80 rfsqsgsgtdftltisslqpediatyccqynsyprafgqtkveik 126

Search completed: January 4, 2002, 18:09:10  
 Job time: 275 sec

SQ Sequence 126 AA;

Query Match 90.7%; Score 507; DB 16; Length 126;

Best Local Similarity 90.7%; Pred. No. 2.7e-30; Mismatches 7; Indels 0; Gaps 0;

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 1 DIQMTQSPSSIASEVGDRTVLTICKASQNVGNVAWYQKPKPKP9QSPK11LYSASYRYSGVPT 60  
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**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2002, 18:05:25 ; Search time 19.66 Seconds  
(without alignments)  
122.475 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQNNIYPLTEGQTKVEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/2/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	518	92.7	126	4	US-08-646-265A-65
2	514	91.9	126	4	US-08-646-265A-43
3	511	91.4	126	4	US-08-646-265A-47
4	510	91.2	126	4	US-08-646-265A-51
5	509	91.1	126	4	US-08-646-265A-57
6	509	91.1	126	4	US-08-646-265A-63
7	507	90.7	126	4	US-08-646-265A-130
8	507	90.7	126	4	US-08-646-265A-53
9	507	90.7	126	4	US-08-646-265A-85
10	507	90.7	126	4	US-08-646-265A-91
11	507	90.7	126	4	US-08-646-265A-109
12	505	90.3	126	4	US-08-646-265A-159
13	503	90.0	126	4	US-08-646-265A-75
14	502.5	89.9	109	2	US-08-602-725-30
15	500	89.4	107	4	US-08-646-265A-131
16	500	89.4	126	4	US-08-646-265A-87
17	495	88.6	126	4	US-08-646-265A-69
18	495	88.6	126	4	US-08-646-265A-77
19	489	87.5	126	4	US-08-646-265A-73
20	488	86.9	107	2	US-07-934-373C-41
21	486	86.9	107	2	US-08-437-642B-41
22	486	86.9	237	2	US-08-463-587A-25
23	486	86.9	237	2	US-08-463-667A-3
24	486	86.9	237	2	US-08-923-854-25
25	486	86.9	237	5	PCT-US91-09133-26
26	485	86.8	126	1	US-08-202-047-13
27	485	86.8	126	1	US-08-202-047-15

28	485	86.8	126	3	US-08-964-690-13	Sequence 13, Appl
29	485	86.8	126	3	US-08-964-690-15	Sequence 15, Appl
30	482	86.2	109	2	US-07-934-373C-3	Sequence 3, Appl
31	482	86.2	109	3	US-08-437-642B-3	Sequence 3, Appl
32	482	86.2	109	5	PCT-US93-07832-3	Sequence 3, Appl
33	482	86.2	126	4	US-08-646-265A-81	Sequence 81, Appl
34	481	86.0	108	3	US-08-974-899-2	Sequence 2, Appl
35	481	86.0	126	1	US-08-202-047-17	Sequence 17, Appl
36	481	86.0	126	3	US-08-964-690-17	Sequence 17, Appl
37	481	86.0	126	3	US-08-964-690-19	Sequence 19, Appl
38	481	86.0	126	3	US-08-964-690-19	Sequence 19, Appl
39	479	85.7	107	2	US-07-934-373C-18	Sequence 18, Appl
40	479	85.7	107	2	US-07-934-373C-43	Sequence 43, Appl
41	479	85.7	107	3	US-08-437-642B-18	Sequence 18, Appl
42	479	85.7	107	3	US-08-437-642B-43	Sequence 43, Appl
43	479	85.7	107	5	PCT-US93-07832-18	Sequence 18, Appl
44	479	85.7	108	3	US-08-974-899-3	Sequence 3, Appl
45	477	85.3	109	2	US-07-934-373C-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-08-646-265A-65  
; Sequence 65, Application US/08646265A  
; Patent No. 6214973  
GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshitiko  
; APPLICANT: SATO, Koh  
; APPLICANT: TSUCHIDA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
; ADDRESS: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265A  
; FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-646-265A-65

Query Match 92.7%; Score 518; DB 4; Length 126;  
Best Local Similarity 93.5%; Pred. No. 5.3e-41;  
Matches 100; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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DB 20 DIOMTQSSSLASASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFYSGVPS 79

OY 61 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107  
DB 80 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNSYPRAFGQGTKEIK 126

RESULT 2  
US-08-646-265A-43  
; Sequence 43, Application US/08646265A  
; Patent No. 6214973  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshiniko  
; APPLICANT: SATO, Koh  
; APPLICANT: TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265A  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELETYPE: 904136  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-646-265A-43

Query Match 91.9%; Score 514; DB 4; Length 126;  
Best Local Similarity 92.5%; Pred. No. 1.2e-40;  
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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DB 20 DIOMTQSSSLASASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFYSGVPS 79

OY 61 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107  
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DB 80 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNSYPRAFGQGTKEIK 126

RESULT 3  
US-08-646-265A-47  
; Sequence 47, Application US/08646265A  
; Patent No. 6214973  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshiniko  
; APPLICANT: SATO, Koh  
; APPLICANT: TSUCHIYA, Masayuki  
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
; TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,265A  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/01763  
; FILING DATE: 19-OCT-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-291078  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WEGNER, Harold C.  
; REGISTRATION NUMBER: 25,258  
; REFERENCE/DOCKET NUMBER: 53466/184  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELETYPE: 904136  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-646-265A-47

Query Match 91.4%; Score 511; DB 4; Length 126;  
Best Local Similarity 91.6%; Pred. No. 2.3e-40;  
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIOMTQSSSLASASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFYSGVPY 60  
DB 20 DIOMTQSSSLASASVGDVVTITCKASQNVGTNVAMVYQOKPGKAPKLLIYSASFYSGVPS 79

OY 61 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNIYPLTFGQGTKEIK 107  
DB 80 RFSGSGCTDFTLTITSSLOPEDFATYYCOQYNSYPRAFGQGTKEIK 126

RESULT 4  
US-08-646-265A-51  
; Sequence 51, Application US/08646265A  
; Patent No. 6214973  
; GENERAL INFORMATION:  
; APPLICANT: OHTOMO, Toshiniko  
; APPLICANT: SATO, Koh



APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-51

Query Match 91.2%; Score 510; DB 4; Length 126;  
Best Local Similarity 91.6%; Pred. No. 2.9e-40;  
Matches 98; Conservative 2; Mismatches 7; Indels 0; Caps 0;

QY 1 DIQMTSPSSLSASVGDVITITCKASQNVGTNVAWYOQKPKAKKLIIYSASFLYSGVPY 60  
|||||  
DB 20 DIQMTSPSSLSASVGDVITITCKASQNVGTNVAWYOQKPKAKKLIIYSASFLYSGVPS 79  
|||||

QY 61 RFGSGSGTDFTLTITSSLOPEDFATYYCQOYNIYPLTFGGGTKEIK 107  
|||||  
DB 80 RFGSGSGTDFTLTITSSLOPEDFATYYCQOYNSYPRAFGGGTKEIK 126  
|||||

RESULT 5  
US-08-646-265A-57  
Sequence 57, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA

ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-57

Query Match 91.1%; Score 509; DB 4; Length 126;  
Best Local Similarity 90.7%; Pred. No. 3.5e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Caps 0;

QY 1 DIQMTSPSSLSASVGDVITITCKASQNVGTNVAWYOQKPKAKKLIIYSASFLYSGVPY 60  
|||||  
DB 20 DIQMTSPSSLSASVGDVITITCKASQNVGTNVAWYOQKPKAKKLIIYSASFLYSGVPS 79  
|||||

QY 61 RFGSGSGTDFTLTITSSLOPEDFATYYCQOYNIYPLTFGGGTKEIK 107  
|||||  
DB 80 RFGSGSGTDFTLTITSSLOPEDFATYYCQOYNSYPRAFGGGTKEIK 126  
|||||

RESULT 6  
US-08-646-265A-63  
Sequence 63, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-63

Query Match 91.1%; Score 509; DB 4; Length 126;  
Best Local Similarity 90.7%; Pred. No. 3.5e-40;  
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVITTCASQNVGTVNVMYQOKPGKAPKLLIYSASFYSGVPY 60  
|||||  
DB 20 DIOMTQSPSSLSASVGDVITTCASQNVGTVNVMYQOKPGKAPKLLIYSASYRSGVPS 79

OY 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGOGTKVEIK 107  
|||||  
DB 80 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGOGTKVEIK 126

RESULT 7  
US-08-646-265A-130  
Sequence 130, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-130

Query Match 90.7%; Score 507; DB 4; Length 107;  
Best Local Similarity 91.6%; Pred. No. 4.6e-40;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDVITTCASQNVGTVNVMYQOKPGKAPKLLIYSASFYSGVPY 60  
|||||  
DB 1 DIOMTQSPSSLSASVGDVITTCASQNVGTVNVMYQOKPGKAPKLLIYSASYRSGVPS 60

OY 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGOGTKVEIK 107  
|||||  
DB 61 RFSGSGSTDFLTITSSLOPEDFATYYCOQYNIYPLTFGOGTKVEIK 107

RESULT 8  
US-08-646-265A-53  
Sequence 53, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-646-265A-53

Query Match 90.7%; Score 507; DB 4; Length 126;  
Best Local Similarity 90.7%; Pred. No. 5.4e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASFYSGVPY 60  
|||||  
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPLTFGGGTVEIK 107  
|||||  
DB 80 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPRAFGGGTVEIK 126

RESULT 9  
US-08-646-265A-85  
; Sequence 85, Application US/08646265A  
; Patent No. 6214973

GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-85

Query Match 90.7%; Score 507; DB 4; Length 126;  
Best Local Similarity 90.7%; Pred. No. 5.4e-40;  
Matches 97; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASFYSGVPY 60  
|||||  
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPLTFGGGTVEIK 107  
|||||  
DB 80 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPRAFGGGTVEIK 126

RESULT 10

US-08-646-265A-91  
; Sequence 91, Application US/08646265A  
; Patent No. 6214973

GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 91:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-91

Query Match 90.7%; Score 507; DB 4; Length 126;  
Best Local Similarity 91.6%; Pred. No. 5.4e-40;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASFYSGVPY 60  
|||||  
DB 20 DIOMTOSPSLSASVGDRTVITTCASONGTNAVWYQOKGKAPKLLIYSASYRSGVPS 79

QY 61 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPLTFGGGTVEIK 107  
|||||  
DB 80 RFSGSGSGTDFLTLLISLQPEDFATYCCOQYNTYPRAFGGGTVEIK 126

RESULT 11  
US-08-646-265A-109  
; Sequence 109, Application US/08646265A  
; Patent No. 6214973

GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE//DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-109

Query Match 90.7%; Score 507; DB 4; Length 269;  
Best Local Similarity 91.6%; Pred. No. 1,2e-39;  
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTCKASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPY 60  
DB 155 DIOMTQSPSSLSASVGDRTTCKASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPS 214

QY 61 RFSSGSGTDFTLTSSLOPEDFATYYCCQYNYIPLTFGGCTKVEIK 107  
DB 215 RFSSGSGTDFTLTSSLOPEDFATYYCCQYNYIPLTFGGCTKVEIK 261

RESULT 12  
US-08-646-265A-59  
Sequence 59, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,265A  
FILING DATE: 09-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01763  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-291078  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE//DOCKET NUMBER: 53466/184  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-265A-59

Query Match 90.3%; Score 505; DB 4; Length 126;  
Best Local Similarity 89.7%; Pred. No. 8,3e-40;  
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTTCKASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPY 60  
DB 20 DIOMTQSPSSLSASVGDRTTCKASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPS 79

QY 61 RFSSGSGTDFTLTSSLOPEDFATYYCCQYNYIPLTFGGCTKVEIK 107  
DB 80 RFSSGSGTDFTLTSSLOPEDFATYYCCQYNYIPLTFGGCTKVEIK 126

RESULT 13  
US-08-646-265A-75  
Sequence 75, Application US/08646265A  
Patent No. 6214973  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, Toshihiko  
APPLICANT: SATO, Koh  
APPLICANT: TSUCHIYA, Masayuki  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
TITLE OF INVENTION: MEDULOBLASTOMA CELLS  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-75

```

```

Query Match          90.0%; Score 503; DB 4; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.3e-39;
Matches 96; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 DIOMTQSPSSLSASVGDRTVITTKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPY 60
    |||||||
DB 20 DIOMTQSPSSLSASVGDRTVITTKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVP 79
    |||||||
QY 61 RFGSGSGTDFTLTSSLOPEDFATYYCQOYNYPLTFEGGTVEIK 107
    |||||||
DB 80 RFGSGSGTDFTLTSSLOPEDIADYFCQOYNSYRAFGGTVEIK 126
    |||||||

```

```

RESULT 14
US-08-602-725-30
Sequence 30, Application US/08602725
Patent No. 5965710
GENERAL INFORMATION:
APPLICANT: BODMER, WALTER F.
APPLICANT: DUBBIN, HELGA
APPLICANT: SMARY, DAVID
APPLICANT: STEWART, LORNA MD
APPLICANT: YOUNG, SUSAN
APPLICANT: BATES, PAUL A.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 1090-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Humanised kappa light chain
US-08-602-725-30

```

```

Query Match          89.9%; Score 502.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 1.2e-39;
Matches 99; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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QY 1 DIOMTQSPSSLSASVGDRTVITTKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVPY 60
    |||||||
DB 1 DIOMTQSPSSLSASVGDRTVITTKASQNVGTNVAWYQKPKAPKLLIYSASFLYSGVP 60
    |||||||
QY 61 RFGSGSGTDFTLTSSLOPEDFATYYCQOYNYPLTFEGGTVEIK 107
    |||||||
DB 61 RFGSGSGTDFTLTSSLOPEDIADYFCQOYNYPLTFEGGTVEIK 108
    |||||||

```

```

RESULT 15
US-08-646-265A-131
Sequence 131, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184

```

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 131:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 107 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-646-265A-131

Query Match 89.4%; Score 500; DB 4; Length 107;  
 Best Local Similarity 89.7%; Pred. No. 2e-39;  
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY	1	DIOMTQSPSSLSASVGDVVTITCKASQNVGNVAMVYQOKPGKAPKLLTYSASFLYSGVPY	60
Db	1	DIOMTQSPSSLSASVGDVVTITCKASQNVGNVAMVYQOKPGKAPKLLTYSASFLYSGVPS	60
QY	61	RFSGSGSGTDFTLTITSSLPEDFATYVCOQYNIYPLTFGCGTKVEIK	107
Db	61	RFSGSGSGTDFTLTITSSLPEDFATYVCOQYNSYPRAFGCGTKVEIK	107

Search completed: January 4, 2002, 18:09:37  
 Job time: 252 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: January 4, 2002, 18:06:20 ; Search time 21.97 Seconds

(without alignments)  
370.991 Million cell updates/sec

Title: US-09-875-221a-11

Perfect score: 559  
Sequence: 1 DIQMTQSPSSLSASVGRVT.....COQNYNYPLRTFGQTKVEIK 107Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries.

Database : PIR\_68:\*

1: pir1:\*\n2: pir2:\*\n3: pir3:\*\n4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	85.0	125	2 S40333	Ig kappa chain V-J
2	473	84.6	125	2 S40349	Ig kappa chain V-J
3	464	83.0	107	2 I69017	anti-HIV1 envelope
4	463	82.8	129	2 S40369	Ig kappa chain - h
5	462	82.6	117	2 S46371	Ig kappa chain V-J
6	461	82.5	123	2 S40313	Ig kappa chain V-J
7	459	82.1	107	2 S36264	Ig kappa chain V
8	459	82.1	108	1 K1H0BN	Ig kappa chain V-I
9	458	81.9	125	2 S40353	Ig kappa chain V-J
10	457	81.8	123	2 S40331	Ig kappa chain - h
11	456	81.6	108	2 B49047	Ig kappa chain V-I
12	455	81.4	117	2 S46376	Ig kappa chain V-J
13	455	81.4	131	2 S40352	Ig kappa chain V-J
14	455	81.4	132	2 S40334	Ig kappa chain - h
15	453.5	81.1	124	2 S40336	Ig kappa chain V-J
16	453	81.0	108	2 S36279	Ig lambda chain V
17	452	80.9	108	2 S36277	Ig lambda chain V
18	451	80.7	107	2 S36269	Ig lambda chain V
19	451	80.7	108	1 K1H0HU	Ig kappa chain V-I
20	451	80.7	127	2 S40367	Ig kappa chain V-J
21	449	80.3	128	2 S46372	Ig light chain var
22	448	80.1	108	2 S19674	Ig kappa chain V-I
23	448	80.1	129	2 S52793	Ig kappa chain V-I
24	447	80.0	108	1 K1H0LY	Ig kappa chain V-I
25	447	80.0	129	2 S40317	Ig kappa chain - h
26	445.5	79.7	107	2 S36275	Ig lambda chain V
27	445	79.6	108	1 K1H0EU	Ig kappa chain V-I
28	444	79.4	108	1 K1H0GL	Ig kappa chain V-I
29	444	79.4	108	1 K1H0WE	Ig kappa chain V-I

30	444	79.4	132	2 S38646	Ig kappa chain V-I
31	443	79.2	129	2 S52789	Ig kappa chain V-I
32	442	79.1	107	2 S36262	Ig lambda chain V
33	440.5	78.8	107	1 K1H0AR	Ig kappa chain V-I
34	440	78.7	125	2 S40316	Ig kappa chain - h
35	440	78.7	125	2 S40350	Ig kappa chain - h
36	440	78.7	127	2 S11240	Ig kappa chain V-I
37	439	78.5	108	1 K1H0AU	Ig kappa chain V-I
38	439	78.5	126	2 S40335	Ig kappa chain V-J
39	439	78.5	130	2 S40368	Ig kappa chain - h
40	438	78.4	108	2 S44122	Ig kappa chain V-I
41	438	78.4	122	2 S40370	Ig kappa chain V-I
42	438	78.4	124	2 S40318	Ig kappa chain V-I
43	437.5	78.3	108	2 S30521	Ig kappa chain V-I
44	437	78.2	108	1 K1H0KU	Ig kappa chain V-I
45	437	78.2	141	2 A49134	Ig kappa chain V-I

## ALIGNMENTS

RESULT 1  
S40333  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40333  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40333  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 475; DB 2; Length 125;  
Best Local Similarity 85.0%; Pred. No. 2e-34;  
Matches 91; Conservative 8; Mismatches 8; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTTCRASQNVGNVAMVYQKPKAPKLLIYSASFLYSGVPY 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 19 DIQMTQSPSSLSASVGRVTTCRASQISSWLAWYQKPKAPKLLIYKASLESQVPS 78  
QY 61 RFSSSGSCTDFTLTITSSLOPEDFATYYCOQNYNYPLRTFGQTKVEIK 107  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 79 RFSSSGSCTDFTLTITSSLOPEDFATYYCOQNYNSYPTFGQTKVEIK 125  
RESULT 2  
S40349  
Ig kappa chain V-J region - human  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1994 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C:Accession: S40349  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PID:9441387  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:33-107/Domain: immunoglobulin homology <IMM>

```

Query Match 84.6%; Score 473; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 3e-34;
Matches 91; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 2 IQMTQSPSSLSASVDRTVITTCASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPYR 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 19 IQLTQSPSSLSASVDRTVITTCRASQGISALAWYQOKPGKAPKLLIYDASSLESQVSR 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 62 FSGSGSGTDFLTITSSLOPEDFAFYCCQYNYITPLTFGQGTKEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 79 FSGSGSGTDFLTITSSLOPEDFAFYCCQFNITPLTFGQGTKEIK 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
169017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (4
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I69017
R:Chn: L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immuno1. Lett. 44, 25-30, 1995
A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A:Reference number: 154563; MUID:95237884
A:Accession: I69017
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:S77140; NID:g913352; PIDN:AMB34102.1; PID:g913353
C:Genetics:
A:Gene: Ig Vkappa
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 464; DB 2; Length 107;
Best Local Similarity 83.2%; Pred. No. 1.5e-33;
Matches 89; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

OY 1 DIQMOTSPSSLSASVGDRTVITTCRASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMOTSPSSLSASVGDRTVITTCRASHDIGSYLAWYQOKPEKAPESLIYASLSQSVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 FRSQSGSGTDFLTITSSLOPEDFAFYCCQYNYITPLTFGQGTKEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 FRSQSGSGTDFLTITSSLOPEDFAFYCCQYNSYITTFGQGTKEIK 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer, immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 463; DB 2; Length 129;
Best Local Similarity 82.2%; Pred. No. 2.3e-33;
Matches 88; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

OY 1 DIQMOTSPSSLSASVGDRTVITTCRASQNVGTNAVYQOKPGKAPKLLIYSASFLYSGVPY 60

```

```

Db      22 DIQMOTSPSSLASVGDRTYITTCRASHVSNHLVWQKRGKAPKLLIYASASLQSGVPS 81
      61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGCGTVEIK 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      82 KFSGSGSGTDFLTITSSLOPEDFATYYCOQYNSPYTFGCGTVEIK 128

RESULT  5
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371: S38645
R:Bensimon, C.; Chastagnet, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene
A:Reference number: S46369; MUID:94313975
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-References: EMBL:427172; NID:9415959; PIDN:CAA81696.1; PID:9415960
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match      82.6%; Score 462; DB 2; Length 117;
Best Local Similarity 82.6%; Pred. No. 2, 5e-33;
Matches 90; Conservative 9; Mismatches 8; Indels 2; Gaps 1;

QY      1 DIQMOTSPSSLASVGDRTYITTCASQNVGTNAVYQKRGKAPKLLIYASASLVSQVP 60
      8 DIQMOTSPSSLASVGDRTYITTCRASRISTWLAWYQKRGKAPKLLIYASASLVSQVP 67
      61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIY--PLTFGCGTVEIK 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      68 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNSPYTFGCGTVEIK 116

RESULT  6
S40313
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40313
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40313
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-References: EMBL:X72423; NID:9441314; PIDN:CAA51091.1; PID:9441315
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match      82.5%; Score 461; DB 2; Length 123;
Best Local Similarity 83.2%; Pred. No. 3, 2e-33;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY      1 DIQMOTSPSSLASVGDRTYITTCASQNVGTNAVYQKRGKAPKLLIYASASLVSQVP 60
      17 DIQMOTSPSSLASVGDRTYITTCRASQGRNDLAWYQKRGKAPKLLIYDASASLVSQVP 76
      61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQYNIYPLTFGCGTVEIK 107
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      77 RFSGSGSGTDFLTITSSLOPEDFATYYCLOQYNGPYTFGCGTVEIK 123

```







F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 81.18; Score 453.5; DB 2; Length 124;  
 Best Local Similarity 82.48; Pred. No. 1.4e-32;  
 Matches 89; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIQWTQSPSSLSASVGDRTTTCASQNVGTNVAWYQKPGKAPKLLITYSASFLYSGVPY 60  
 |||:||||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 16 DIQLTQSPSPFLSASVGDRTTTCRASQGISSTYLAHYQKPGKAPKLLITYASTLQSGVPS 75  
 QY 61 RFSGSGSGTDFTLTITSSLOPEDFATYCCQYNIY-PLTFGGGTKEIK 107  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 76 RFSGSGSGTEFSLTITSSLOPEDFATYCCQQLNTYPPWTFGGGTKEIK 123

Search completed: January 4, 2002, 18:10:05  
 Job time: 225 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:41 ; Search time 15.29 Seconds  
(without alignments)  
256.582 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559

Sequence: 1 DIQMTQSPSSLSASVGRVT.....CQQVNIYPLTFGGTKVEIK 107

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459	82.1	108	1	KV1V_HUMAN
2	451	80.7	108	1	KV1H_HUMAN
3	447	80.0	108	1	KV1M_HUMAN
4	445	79.6	108	1	KV1E_HUMAN
5	444	79.4	108	1	KV1G_HUMAN
6	444	79.4	108	1	KV1R_HUMAN
7	440.5	78.8	107	1	KV1D_HUMAN
8	440	78.7	108	1	KV1B_HUMAN
9	439	78.5	108	1	KV1A_HUMAN
10	437	78.2	108	1	KV1P_HUMAN
11	434	77.6	108	1	KV1S_HUMAN
12	432	77.3	108	1	KV1O_HUMAN
13	430	76.9	108	1	KV1Q_HUMAN
14	428	76.6	108	1	KV1W_HUMAN
15	428	76.6	129	1	KV1V_HUMAN
16	424	75.8	108	1	KV1K_HUMAN
17	422	75.5	108	1	KV1C_HUMAN
18	421	75.3	108	1	KV1A_HUMAN
19	420	75.1	108	1	KV1N_HUMAN
20	417	74.6	108	1	KV1E_HUMAN
21	414	74.1	117	1	KV1J_HUMAN
22	413	73.9	117	1	KV1I_HUMAN
23	407	72.8	129	1	KV1X_HUMAN
24	403	72.1	149	1	KV5A_MOUSE
25	392.5	70.2	109	1	KV1T_HUMAN
26	392	70.1	112	1	KV1U_HUMAN
27	391	69.9	108	1	KV5J_MOUSE
28	390.5	69.9	129	1	KV3H_HUMAN
29	389.5	69.7	129	1	KV3I_HUMAN
30	387	69.2	108	1	KV5O_MOUSE
31	386	69.1	108	1	KV5T_MOUSE
32	384	68.7	108	1	KV5S_MOUSE
33	383.5	68.6	109	1	KV3D_HUMAN

34	382.5	68.4	129	1	KV3M_HUMAN
35	382	68.3	108	1	KV5D_MOUSE
36	381	68.2	134	1	KV4C_HUMAN
37	380.5	68.1	109	1	KV3B_HUMAN
38	380	68.0	128	1	KV5E_MOUSE
39	378.5	67.7	109	1	KV3F_HUMAN
40	378	67.6	108	1	KV5P_MOUSE
41	377	67.4	114	1	KV4A_HUMAN
42	377	67.4	136	1	KV5B_MOUSE
43	376	67.3	108	1	KV5L_MOUSE
44	376	67.3	108	1	KV5R_MOUSE
45	375.5	67.2	109	1	KV3E_HUMAN

## ALIGNMENTS

RESULT	1	STANDARD	PRT	108 AA.
KV1V_HUMAN				
ID	KV1V_HUMAN			
AC	P04430			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG KAPPA CHAIN V-I REGION BAN.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=86174817; PubMed=3083240;			
RA	Dwulet F.E., O'Connor T.P., Benson M.D.;			
RT	"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";			
RL	Mol. Immunol. 23:73-78(1986).			
DR	PIR: A01878; KIHUBN.			
DR	HSSP: P80362; 1WTL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_1.			
DR	SMART: SM00406; IgV_1.			
KW	Immunoglobulin V region; Amyloid.			
FT	DOMAIN 1 23			FRAMEWORK 1.
FT	DOMAIN 24 34			FRAMEWORK 2.
FT	DOMAIN 35 49			FRAMEWORK 3.
FT	DOMAIN 50 56			FRAMEWORK 4.
FT	DOMAIN 57 88			COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN 89 97			COMPLEMENTARITY-DETERMINING 4.
FT	DOMAIN 98 107			FRAMEWORK 4.
FT	DISULFID 23 88			BY SIMILARITY.
FT	NON_TER			
SO	SEQUENCE	108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;		

Query Match 82.1%; Score 459; DB 1; Length 108;  
Best Local Similarity 83.2%; Pred. No. 1.1e-41;  
Matches 89; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY	1	DIQMTQSPSSLSASVGRVTITCKRASNQVGNVAMYOQPKAPKLLIYSASFYSGVPY 60
DB	1	DIQMTQSPSSLSASVGRVITTCRASQSVNVVAMFOQPKAPKSLIYDASTLQSGVPS 60
QY	61	RFSGSGSTDTFTLTITSSLPEDFATYYCQNYNITPLTFGGTKVEIK 107
DB	61	NETSSGSGTDFILRTISLPEDFATYYCQYNSYPTFGGTKVQIK 107

RESULT	2	STANDARD	PRT	108 AA.
ID	KV1H_HUMAN			
AC	P01600			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein HAU): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01868; KIHUHU.
DR HSSP: P80362; IGMTL.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IqV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 98 107 FRAMEWORK 4.
FT NON_TER 23 88 BY SIMILARITY.
FT SEQUENCE 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.7%; Score 451; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 7.8e-41;
Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDVTTTCASQNVGVNANYOQPKAPRLIYASFLYSGVPY 60
DB 1 DIQMTPSSLSASVGDVTTTCASQNVGVNANYOQPKAPRLIYASFLYSGVPY 60
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107

RESULT 3
KV1F_HUMAN STANDARD; PRT; 108 AA.
ID KV1F_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.

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DR PIR: A01871; KIHULY.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IqV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 98 107 FRAMEWORK 4.
FT NON_TER 23 88 BY SIMILARITY.
FT SEQUENCE 108 AA; 11834 MW; 73993A95431434A CRC64;

Query Match 80.0%; Score 447; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 2.1e-40;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDVTTTCASQNVGVNANYOQPKAPRLIYASFLYSGVPY 60
DB 1 DIQMTPSSLSASVGDVTTTCASQNVGVNANYOQPKAPRLIYASFLYSGVPY 60
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107
DB 61 RFSGSGSTDFLTITSLQPEDFATYVCOQYNIYPLTFGQGTKEIK 107

RESULT 4
KV1F_HUMAN STANDARD; PRT; 108 AA.
ID KV1F_HUMAN
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION EU.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RT Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RT Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR: A01866; KIHUHU.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq; 1.
DR SMART: SM00406; IqV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 FRAMEWORK 3.
FT DOMAIN 6 88 FRAMEWORK 4.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.

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RT protein.";  
 RC Eur. J. Biochem. 49:377-391(1974).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR: A01864; KIHUAD.  
 DR HSP: P80362; 1WTL.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 FT CARBOXD 28 28 N-LINKED (GLCNAC. . .).  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C346 CRC64;  
 Query Match 78.8%; Score 440.5; DB 1; Length 107;  
 Best Local Similarity 78.5%; Pred. No. 9.8e-40;  
 Matches 84; Conservative 12; Mismatches 10; Indels 1; Gaps 1;  
 Oy 1 DIQMTSPSSLSASVGDPRVTITCKASQNVGTNAVWYQOKPKAPRLIYSASFLYSGVPY 60  
 Db 1 DIQMTGSPSTLASVGDPRVATTCRASQNISSMLAWYQOKPKAPKVLTKSSLESQVPS 60  
 Oy 61 RFSSGSGCTDFTLTITSSLOPEDFATYTCQQYNIYPLTFGGCTKVEIK 107  
 Db 61 RFSSGSGCTDFTLTITSSLOPEDFATYTCQQYNTF-FTFGPGTKVDIK 106  
 RESULT 8  
 KVIY\_HUMAN STANDARD; PRT; 108 AA.  
 AC P80362;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WAT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95086080; Pubmed=793911;  
 RA Huang D.-B., Chang C.-H., Almsworth C., Bruenger A.T., Eulitz M.,  
 RA Solomon A., Stevens F.J., Schiffer M.;  
 RT "Comparison of crystal structures of two homologous proteins:  
 RT structural origin of altered domain interactions in immunoglobulin  
 RT light-chain dimers";  
 RL Biochemistry 33:14848-14857(1994).  
 RN [2]  
 RP SEQUENCE OF 1-35.  
 RX MEDLINE=81267384; Pubmed=6167731;  
 RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
 RA Popp R.A., Solomon A.;  
 RT "Characterization and preliminary crystallographic data on the VL-  
 RT related fragment of the human kappa Bence Jones protein Wat.";  
 RL J. Mol. Biol. 147:185-193(1981).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PDB: 1WTL; 01-NOV-94.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT DOMAIN 2 34 FRAMEWORK 2.  
 FT DOMAIN 3 49 FRAMEWORK 3.  
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	Matches	86:	Conservative *	5:	Mismatches	16:	Indels	0:	Gaps	0:	
OY	1 DIOMTQSPSSLSASVGDRTYTCTKASQNVTNVAMYOQPKGAPKLLIYSASFLYSGVPY	60	:								
Dd	1 DIOMTQSSTSLASVAGDVRTITTCRASODISDIYNWYOQPKGAPKLLIDASNLEGVPS	60	:								
OY	61 RFSGGSGTDFTLTISSLOPEDFATRYCOQNYNIPLTFEGGRKEVKR	107	:								
Dd	61 RFGSGSGAHFFTTTSSLQEDPATRYCCOXYDLPTWTGQGTRKEVKR	107	:								
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	RESULT 10	KVII_HUMAN	STDARD:	PRT:	108 AA.						
ID	AC P01604;	KVII_HUMAN	STDARD:	PRT:	108 AA.						
DT	21-JUL-1986 (Rel. 01, Created)										
DT	21-JUL-1986 (Rel. 01, Last sequence update)										
DT	15-JUL-1999 (Rel. 38, last annotation update)										
DE	IG KAPPA CHAIN V-I REGION KUE.										
OS	Homo sapiens (Human).										
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
NC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.										
OX	NCL_TaxId=9606;										
RN	[!]										
RP	SEQUENCE.										
RA	MEDLINE=79237924; PubMed=112021;										
RX	Eultiz M., Kley H.-P., Zeitler H.-J.;										
RT	"The primary structure of the Bence-Jones protein from Kue. The amino acid sequence of the variable part of a human I-chain of the kappa-type.";										
RL	Hope-Seyler's Z. Physiol. Chem. 360:725-734(1979). -I-MISCCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER. PIR: A01870; KIHUKU.										
DR	HSSP: P01607; IRRI.										
DR	IInterpro: IPRO03006; IG_MHC.										
DR	IInterPro: IPPRO03596; IG_V.										
DR	Pfam: PF00047; Ig_1.										
KM	SMART: SM00406; IgV_1.										
FM	Immunoglobulin V region; Bence-Jones protein.										
FY	DOMAIN 1 23 FRAMEWORK 1.										
FE	DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.										
FE	DOMAIN 35 49 FRAMEWORK 2.										
FE	DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.										
FE	DOMAIN 57 88 FRAMEWORK 3.										
FE	DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.										
FE	DOMAIN 98 107 FRAMEWORK 4.										
FE	DISUFID 23 88 BY SIMILARITY.										
FN	NON_TER 108 108										
SQ	SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;										
<hr/>											
	Query Match	78.2%;	Score 437;	DB 1;	Length 108;						
	Best Local Similarity	77.6%;	Pred. No. 2.3e-39;								
	MATCHES 83: Conservative 12; Mismatches 12; Indels 0; Gaps 0;										
OY	1 DIOMTQSPSSLSASVAGDVRTITTCRASQNVTNVAMYOQPKGAPKLLIYSASFLYSGVPY	60	:								
Dd	1 DIOMTQSSTQSAVGDRVITICTCRASQSIINIMLAWYOQPEAKPKLLIKASTLEGVPS	60	:								
OY	61 RFSGGSGTDFTLTISSLOPEDFATRYCOQNYNIPLTFEGGRKEVKR	107	:								
Dd	61 RFSGGSGETFLTTLNSLDPPDFATRYCQXSRYPYTGOGTKELDK	107	:								
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	RESULT 11	KVIP_HUMAN	STDARD:	PRT:	108 AA.						
ID	AC P01608;	KVIP_HUMAN	STDARD:	PRT:	108 AA.						
DT	21-JUL-1986 (Rel. 01, Created)										
DT	21-JUL-1986 (Rel. 01, Last sequence update)										
DT	15-JUL-1999 (Rel. 38, last annotation update)										
DE	IG KAPPA CHAIN V-I REGION KOY.										
OS	Homo saplens (Human).										

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=683632076; PubMed=5595110;  
 RA Hilschmann N.;  
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and  
 RT Cum.)";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).  
 RL [2]  
 RP REVISIONS TO 39 AND 41.  
 RA Hilschmann N., Bernikol H.U., Hess M., Langer B., Ponslingl H.,  
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;  
 RL (In) Franek F., Shugar D. (eds.);  
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,  
 RL New York (1969)  
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -I- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.  
 DR PIR: A01874; KIHURY.  
 DR HSSP: P80362; 1WTL.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; IgV\_1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK 1.  
 FT 24 34 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 35 49 FRAMEWORK 2.  
 FT 50 56 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 57 88 FRAMEWORK 3.  
 FT 89 97 COMPLEMENTARITY-DETERMINING 3.  
 FT DOMAIN 98 107 FRAMEWORK 4.  
 FT DISULFD 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;  
 Query Match 77.6%; Score 434; DB 1; Length 108;  
 Best Local Similarity 78.5%; Pred. No. 4.8e-39;  
 Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 DIQMQSPSSASVGVDRYTITCKASQNVGTWVWVQOKPKGKAPLLIYSASFLYGVVPY 60  
 Db 1 DIQMQSPSSLASVSGDRITITCQASQDLSIFLNMYYQKPKGKAPRLILLYDASKLEAGVPS 60  
 QY 61 RSSGSGGTDEFTLLTSSLOPEDFATRYCCQYNIYPLFEGQGTKEVR 107  
 Db 61 RSSGSGGTDEFTFTTSSLOPEDIATRYCCQDFNLPLTFEGGTRKVPFK 107  
 RESULT 12  
 KVIS\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01611;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION WES.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=81092279; PubMed=6778806;  
 RA Kretzlin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolysate of a protein by  
 RT high-pressure liquid chromatography. The primary structure of a  
 RT monoclonal I-chain of k-type, subgroup I (Bence-Jones Protein  
 RT Wes).";  
 RT Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01877; KIH0WS.  
DR HSSP: P80362; 1MTL.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam: PF00047; Iq; 1.  
DR SMART: SM00406; Iq; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 3 49 FRAMEWORK 2.  
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 6 57 FRAMEWORK 3.  
FT DOMAIN 7 88 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
SO SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 77.3%; Score 432; DB 1; Length 108;  
Best Local Similarity 79.4%; Pred. No. 7.8e-39;  
Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
QY 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTNAVYQOKPKAPRLIYASFLYSGVPY 60  
DB 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTNAVYQOKPKAPRLIYASFLYSGVPY 60  
OY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQYNIYPLTFGOGTKVEIK 107  
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCOQYNIYPLTFGOGTKVEIK 107

RESULT 13  
KV10\_HUMAN STANDARD: PRT: 108 AA.  
ID KV10\_HUMAN  
AC P01609;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION SCW.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75059271; PubMed=4435756;  
RA Eulitz M., Hilschmann N.;  
RT "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.); II: The chymotryptic peptides and the complete amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01875; KIH0SW.  
DR HSSP: P01607; IREI.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam: PF00047; Iq; 1.  
DR SMART: SM00406; Iq; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 3 49 FRAMEWORK 2.  
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 6 57 FRAMEWORK 3.  
FT DOMAIN 7 88 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108

SO SEQUENCE 108 AA; 11764 MW; 32CECDDDF9644414 CRC64;

Query Match 76.9%; Score 430; DB 1; Length 108;  
Best Local Similarity 76.6%; Pred. No. 1.3e-38;  
Matches 82; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTNAVYQOKPKAPRLIYASFLYSGVPY 60  
DB 1 DIQMTQSPSSLSASVGRVTITCKASQNVGTNAVYQOKPKAPRLIYASFLYSGVPY 60  
OY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQYNIYPLTFGOGTKVEIK 107  
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCOQYNIYPLTFGOGTKVEIK 107

RESULT 14  
KV10\_HUMAN STANDARD: PRT: 108 AA.  
ID KV10\_HUMAN  
AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION REI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=809329;  
RA Palm W., Hilschmann N.;  
RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=76039968; PubMed=1182131;  
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";  
RL Biochemistry 14:4943-4952(1975).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR: A01873; KIH0RE.  
DR PDB: IREI; 17-FEB-84.  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003596; Iq\_V.  
DR Pfam: PF00047; Iq; 1.  
DR SMART: SM00406; Iq; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23 FRAMEWORK 1.  
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 3 49 FRAMEWORK 2.  
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 5 56 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 6 57 FRAMEWORK 3.  
FT DOMAIN 7 88 FRAMEWORK 4.  
FT DISULFID 23 88  
FT STRAND 4 7  
FT STRAND 10 13  
FT TURN 15 16  
FT STRAND 19 25  
FT TURN 30 31  
FT STRAND 33 38  
FT TURN 40 41  
FT STRAND 45 49  
FT TURN 50 52

FT STRAND 53 54  
 FT TURN 56 57  
 FT TURN 60 61  
 FT STRAND 62 67  
 FT TURN 68 69  
 FT STRAND 70 75  
 FT HELIX 80 82  
 FT STRAND 85 90  
 FT STRAND 98 98  
 FT STRAND 102 106  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11922 MW; 9E8143E1188BCE2A CRC64;

Query Match 76.6%; Score 428; DB 1; Length 108;  
 Best Local Similarity 78.3%; Pred. No. 2.1e-38;  
 Matches 83; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60  
 DB 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60  
 QY 61 RFSGSGSGTDEFTLTITSLQPEDFATYYCQOYNIVPLTEGQGTVEIK 106  
 DB 61 RFSGSGSGTDEFTLTITSLQPEDFATYYCQOYNIVPLTEGQGTVEIK 106

RESULT 15

ID KVIW\_HUMAN STANDARD; PRT; 129 AA.

AC P04431;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DF 13-AUG-1987 (Rel. 05, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DI IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID-9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-85014148; PubMed-6091049;  
 RA Klobbeck H.G., Combrato G., Zachau H.G.;  
 RT "Immunoglobulin genes of the kappa light chain type from two human  
 lymphoid cell lines are closely related";  
 RL Nucleic Acids Res. 12:6995-7006(1984).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL: X00965; CAA25477.1; ALT\_TERM.  
 DR PTR: A01883; KIHUK.  
 DR HSSP: P01607; 1RET.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 129  
 FT DOMAIN 23 45  
 FT DOMAIN 46 56  
 FT DOMAIN 57 71  
 FT DOMAIN 72 78  
 FT DOMAIN 79 110  
 FT DOMAIN 111 119  
 FT DOMAIN 120 129  
 FT DISULFID 45 110  
 BY SIMILARITY.

FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFAFC2P9 CRC64;

Query Match 76.6%; Score 428; DB 1; Length 129;  
 Best Local Similarity 79.4%; Pred. No. 2.5e-38;  
 Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 60  
 DB 23 DIQMTQSPSSLSASVGDGVITTCASQNVGTNVAWYQKPGKAPKLLIYASFLYSGVPY 82  
 QY 61 RFSGSGSGTDEFTLTITSLQPEDFATYYCQOYNIVPLTEGQGTVEIK 107  
 DB 61 RFSGSGSGTDEFTLTITSLQPEDFATYYCQOYNIVPLTEGQGTVEIK 107

Search completed: January 4, 2002, 18:14:37  
 Job time: 296 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:08:31 ; Search time 37.65 Seconds  
(without alignments)  
415.701 Million cell updates/sec

Title: US-09-875-221A-11

Perfect score: 559

Sequence: 1 DIOMTQSPSSLSASVGDVRT.....COQYNLYPLTFGGTKEIK 107

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_17.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	80.1	108	4 Q9UL70	Q9u170 homo sapien
2	441	78.9	108	4 Q9UL77	Q9u177 homo sapien
3	432	77.3	108	4 Q9UL79	Q9u179 homo sapien
4	420.5	75.2	107	4 Q9UL81	Q9u181 homo sapien
5	399	71.4	108	4 Q9UL83	Q9u183 homo sapien
6	392.5	70.2	109	4 Q9UL85	Q9u185 homo sapien
7	384	68.7	214	11 Q9RIAS	Q9u185 mus musculu
8	379.5	67.9	109	4 Q9UL78	Q9u178 homo sapien
9	374	66.9	298	11 Q9OYF0	Q9u178 mus musculu
10	372	66.5	107	11 Q9UL84	Q9u184 mus musculu
11	353.5	63.2	109	4 Q9UL86	Q9u186 mus musculu
12	343	61.4	99	11 Q9UL74	Q9u174 mus musculu
13	342.5	61.3	106	5 Q9UL10	Q9u174 schistosoma
14	334	59.7	107	11 Q9ER29	Q9u176 mus musculu
15	325.5	58.2	238	11 Q9NM37	Q9u176 mus musculu
16	306	54.7	101	11 Q9UL78	Q9u178 mus musculu
17	305	54.6	103	11 Q9UL80	Q9u180 mus musculu
18	298	53.3	97	11 Q9UL76	Q9u176 mus musculu
19	294	52.6	109	6 Q9N0W5	Q9u176 mus musculu

20	292.5	52.3	104	11 Q9UL82	Q9u182 mus musculu
21	288	51.5	114	4 Q9UL80	Q9u180 mus sapien
22	214	38.3	107	4 Q9UL82	Q9u182 mus sapien
23	208.5	37.3	107	4 Q9NSD6	Q9u186 mus sapien
24	196.5	35.2	235	11 Q9NM11	Q9u181 mus musculu
25	178	31.8	130	4 Q9NP29	Q9u129 mus sapien
26	154.5	27.6	109	11 Q9ET13	Q9u183 mus musculu
27	151.5	27.1	334	13 Q9IB05	Q9u185 mus musculu
28	149.5	26.7	337	13 Q9TB02	Q9u182 mus musculu
29	143	25.6	93	4 Q9UL76	Q9u176 mus sapien
30	142	25.4	135	4 Q9HS24	Q9u176 mus sapien
31	135.5	24.2	484	11 Q9ULA6	Q9u186 mus musculu
32	134	24.0	342	13 Q9IB00	Q9u180 mus musculu
33	130	23.3	123	11 Q61A23	Q6u123 mus musculu
34	121.5	21.7	337	13 Q9IA24	Q9u184 mus musculu
35	120	21.5	320	13 Q9IA29	Q9u184 mus musculu
36	118.5	21.2	509	11 Q9QX57	Q9u182 mus musculu
37	118.5	21.2	513	11 P97797	Q9u182 mus musculu
38	112.5	20.1	122	4 Q9PE604	Q9u182 mus musculu
39	112.5	20.1	137	4 Q9UDR1	Q9u182 mus musculu
40	112.5	20.1	509	11 Q08907	Q9u182 mus musculu
41	112	20.0	318	13 Q9IB03	Q9u183 mus musculu
42	111.5	19.9	339	13 Q9IAY8	Q9u183 mus musculu
43	110.5	19.8	122	4 Q9PE603	Q9u182 mus musculu
44	109.5	19.6	332	13 Q9IB08	Q9u182 mus musculu
45	108	19.3	118	4 Q9UL72	Q9u172 mus sapien

## ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	108 AA.
Q9UL70	Q9UL70			
AC	Q9UL70			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-I-SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF035044; AAD56280.1; -			
DR	HSSP: P01607; IREL.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam: PF00047; Ig_V.			
DR	SMART: SM00406; IGV; 1.			
FT	NON_TER 1			
FT	NON_TER 108			
SO	SEQUENCE 108 AA; 11633 MW; B7BDC3E41FCCA37 CRC64;			
Query Match	80.1%; Score 448; DB 4; Length 108;			
Best Local Similarity	81.3%; Pred. No. 6,1e-41;			
Matches	87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;			
QY	1 DIOMTQSPSSLSASVGDVRTITCKASQNGFNVAWYQOKGKAPKLLIYSASFYSGVPY 60			
DB	1 DIOMTQSPSSLSASVGDVRTITCKASQNGFNVAWYQOKGKAPKLLIYSASFYSGVPY 60			
QY	61 RFGSGSGVDFTLITLISLQPEDFATYYCOQYNLYPLTFGGTKEIK 107			

Db 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

## RESULT 2

ID Q9UL77 PRELIMINARY: PRT: 108 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035037; AAD56273.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; Igv; 1.

FT NON\_TER 1

FT NON\_TER 108

FT NON\_TER 108

SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 78.9%; Score 441; DB 4; Length 108;

Best Local Similarity 81.3%; Pred. No. 3.5e-40;

Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Db 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Qy 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

Db 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

## RESULT 3

ID Q9UL79 PRELIMINARY: PRT: 108 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035035; AAD56271.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; Igv; 1.

FT NON\_TER 1

FT NON\_TER 108

FT NON\_TER 108

SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 77.3%; Score 432; DB 4; Length 108;

Best Local Similarity 78.5%; Pred. No. 3.2e-39;

Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Db 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Qy 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

Db 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

## RESULT 4

ID Q9UL81 PRELIMINARY: PRT: 107 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035033; AAD56269.1; -

DR HSSP: P80362; IWTI.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; Igv; 1.

FT NON\_TER 1

FT NON\_TER 107

FT NON\_TER 107

SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.2%; Score 420.5; DB 4; Length 107;

Best Local Similarity 78.5%; Pred. No. 5.6e-38;

Matches 84; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Db 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Qy 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

Db 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

## RESULT 5

ID Q9UL83 PRELIMINARY: PRT: 108 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RP SEQUENCE FROM N.A.

RA MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

DR EMBL: AF035035; AAD56271.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; Igv; 1.

FT NON\_TER 1

FT NON\_TER 108

FT NON\_TER 108

SEQUENCE 108 AA; 11787 MW; DB5845F19724FBAE CRC64;

Query Match 77.3%; Score 432; DB 4; Length 108;

Best Local Similarity 78.5%; Pred. No. 3.2e-39;

Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Db 1 DIQMTQSPSSLSASVGDVNTTCRAQNVGTNAVYQOKPGKAPKLLIYASFLYSGVPY 60

Qy 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107

Db 61 RFSGSGSTDEFTLTITSSLOPEDVATYCOQYNAPRTGPGTKLEIK 107











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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:10 ; Search time 38.05 Seconds  
(without alignments)  
25.308 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPYTKSPNRESC 13

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq.1101:\*

1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT:\*

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18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	106	9 AAP81028	C region of L chain
2	70	100.0	106	14 AAP41687	Undefined ORF1 enc
3	70	100.0	106	14 AAP43686	Human kappa consta
4	70	100.0	106	18 AAP37347	Immunoglobulin C-k
5	70	100.0	106	19 AAP59622	Anti-RSV F protein
6	70	100.0	106	19 AAP48649	Constant region of
7	70	100.0	106	22 AAP04072	Interleukin recept
8	70	100.0	107	19 AAP40578	Human kappa CL dom
9	70	100.0	107	20 AAP50152	Human kappa light
10	70	100.0	107	20 AAP08745	Human kappa-CL dom
11	70	100.0	107	20 AAP92425	Human kappa protei

12	70	100.0	107	21 AAP27000	Human kappa CL dom
13	70	100.0	107	22 AAP62265	Light chain constr
14	70	100.0	108	20 AAP70802	Amino acid sequenc
15	70	100.0	108	21 AAP92191	Human IgG1 kappa d
16	70	100.0	143	10 AAP93559	Sequence of human
17	70	100.0	143	22 AAG75780	Human colon cancer
18	70	100.0	201	20 AAP29770	P-selectin ligand
19	70	100.0	213	17 AAP04301	Antibody fusion pr
20	70	100.0	213	17 AAP05830	Humanised M291 ant
21	70	100.0	213	22 AAP83157	Ganglioside GM2 an
22	70	100.0	214	14 AAP30776	H5216-158 murine a
23	70	100.0	214	14 AAP43338	Completely humanis
24	70	100.0	214	17 AAP05828	Humanised ID10 ant
25	70	100.0	214	17 AAP00373	Anti-CD18 chimeric
26	70	100.0	214	18 AAP45517	NANUC-2 light chain
27	70	100.0	214	18 AAP34504	Light chain of hum
28	70	100.0	214	18 AAP34506	Light chain of ful
29	70	100.0	214	18 AAP07615	Ulcerative colitis
30	70	100.0	214	19 AAP64671	Human UC PANCA mon
31	70	100.0	214	19 AAP49815	Amino acid sequenc
32	70	100.0	214	20 AAP34039	NANUC-2 antibody 1
33	70	100.0	214	20 AAP30202	Light chain sequen
34	70	100.0	214	20 AAP08754	Human antibody huf
35	70	100.0	214	20 AAP08599	Anti-human TNF- $\alpha$ lp
36	70	100.0	214	20 AAP08600	JPL1127855 Seg ID
37	70	100.0	214	20 AAP06842	Seq ID No.10 of JP
38	70	100.0	214	20 AAP95615	Humanized anti-CD1
39	70	100.0	214	20 AAP30632	Recombinant human1
40	70	100.0	214	21 AAP29407	Human monoclonal a
41	70	100.0	214	21 AAP93735	The kappa chain of
42	70	100.0	214	21 AAP57337	UC PANCA Mab NANUC
43	70	100.0	215	22 AAP65777	Rhucab CD18 light
44	70	100.0	215	18 AAP07616	Ulcerative colitis
45	70	100.0	215	19 AAP64673	Human UC PANCA mon

#### ALIGNMENTS

RESULT 1	
ID AAP81028	standard; protein; 106 AA.
XX	
AC AAP81028:	
XX	
DT 17-OCT-1990	(first entry)
XX	
DE C region of L chain (chi) of human antibody.	
XX	
KW mouse-human chimeric antibody ; anticancer agent;	
KW human common acute lymphocytic leukaemia; ss.	
XX	
OS Homo sapiens.	
XX	
PN EP255694-A.	
XX	
PD 10-FEB-1988.	
XX	
PF 29-JUL-1987;	87EP-0110994.
XX	
PR 30-JUL-1986;	86JP-0177809.
XX	
PA (TEIJ ) TEIJIN KK.	
XX	
PI Nishimura Y, Ichikawa Y, Kudo A, Watanabe T;	
XX	
DR WPI; 1988-037653/06.	
XX	
PT Mouse-human chimera antibody -	
PT used for diagnosis and therapy of human common acute lymphocytic	
PT leukaemia	
XX	
PS Disclosure; ; P; English.	

XX CC The chimeric antibody comprises a C region of human origin linked  
CC to a V region of mouse origin in both the L and H chains. The mouse  
CC -derived V region is opt. reactive with human common lymphocytic  
CC leukaemia antigen.  
CC See also AAN81358-9, AAN81360, AAN81362-6 and AAP81025-7.  
XX  
SQ Sequence 106 AA:  
  
Query Match 100.0%; Score 70; DB 9; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPVTKSPFNRGEC 13  
Db 94 ssptvksfngrec 106  
|||||  
RESULT 2  
AAR41687  
ID AAR41687 standard; Protein: 106 AA.  
XX  
AC AAR41687;  
XX  
DT 20-OCT-1993 (first entry)  
XX  
DE Undefined ORF1 encoded by plasmid pAH4611.  
XX  
KW Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;  
KW chain; variable; constant; region; anti-human; transferrin; receptor;  
KW antibody; brain; capillary; endothelial cell; conjugate; epilepsy;  
KW neuropharmacological; diagnostic; agent; tumour; AIDS; stroke;  
KW Parkinsons disease; Alzheimers disease.  
XX  
OS Synthetic.  
XX  
PN W09310819-A.  
PD 10-JUN-1993.  
XX  
PE 24-NOV-1992; 92WO-US10206.  
XX  
PR 26-NOV-1991; 91US-0800458.  
XX  
PA (ALKE-) ALKERMES INC.  
XX  
PI Friden PM;  
XX  
DR WPI: 1993-196742/24.  
DR N-PSDB; AAQ43845.  
XX  
PT Antibody conjugates specific for transferrin receptor - used  
PT for diagnosis and treatment of cancer, AIDS and neurological  
PT disorders  
XX  
PS Disclosure; Fig 13H; 151pp; English.  
XX  
CC The sequences given in AAR41686-87 represent proteins encoded by the  
CC expression vector pAH4611. This vector was produced from the plasmid  
CC pAG4270. pAG4270 is the expression vector for the light chain  
CC variable region (VL) of the antibody 128.1 which was obtained by PCR  
CC with leader/J region priming (see also AAQ43842). The vector also  
CC contains an ampicillin resistance gene, a gpt (mycophenolic acid  
CC resistance) selected marker, an immunoglobulin H enhancer and an  
CC intron for V-constant region splicing. Transcription of the CH gene  
CC is from the VH promoter of the murine 27.44 gene. The cloning of  
CC the 128.1 VL region was accomplished in two stages with the production  
CC of plasmid pSV4271 as an intermediate vector which lacks the promoter  
CC region. This plasmid was used in conjunction with pAH4602 in the  
CC production of the chimeric antibody 128.1. 128.1 is an anti-human  
CC transferrin receptor antibody which binds to the transferrin receptor  
CC on brain capillary endothelial cells. This antibody may be used in a

CC conjugate in which it is linked to a neuropharmacological or diagnostic  
CC agent. The conjugate may be used to treat or prevent neurological  
CC disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and  
CC Alzheimers disease. It may also be used for diagnostic methods.  
XX  
SQ Sequence 106 AA:  
  
Query Match 100.0%; Score 70; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SSPVTKSPFNRGEC 13  
Db 94 ssptvksfngrec 106  
|||||  
RESULT 3  
AAR43686  
ID AAR43686 standard; Protein: 106 AA.  
XX  
AC AAR43686;  
XX  
DT 25-MAY-1994 (first entry)  
XX  
DE Human kappa constant domain as encoded by pHCW-KR.  
XX  
KW Human; immunoglobulin; constant; region; humanised; P-selectin; light;  
KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;  
KW monoclonal; Pbl.3; CDR; complementarily determining region; leukocyte;  
KW expression vector; coexpression; pHCW-1748RLA-gammaCI-dhfr; epitope;  
KW pHCW-1748RLA-KR-neo; Pbl.3/humanised version A; vascular endothelium;  
KW pHCW-1747CH-gammaCI-neo; pHCW-1747-CL-KR-neo; Pbl.3 chimera;  
KW acute lung injury; ischaemia reperfusion injury; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN W09321956-A.  
PD 11-NOV-1993.  
XX  
PE 04-MAY-1993; 93WO-US04274.  
XX  
PR 05-MAY-1992; 92US-0880196.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Chestnut RW, Paulson JC, Polley MJ;  
XX  
DR WPI: 1993-368423/46.  
DR N-PSDB; AAQ51548.  
XX  
PT Anti-P-selectin antibody for ischaemia acute lung injury treatment -  
PT useful to treat inflammation and pathological conditions of  
PT intercellular adhesion by competitive inhibition assays  
XX  
PS Example 10; Fig 10; 82pp; English.  
XX  
CC The sequences given in AAR43685-86 represent human immunoglobulin  
CC constant regions which were used in the production of the humanised  
CC P-selectin blocking antibody, along with the heavy and light chain  
CC variable region coding sequences of the murine monoclonal antibody  
CC Pbl.3, given in AAR43687-88. The CDRs from Pbl.3 heavy and light  
CC chains were substituted for the CDRs of human heavy and light chains.  
CC The humanised variable regions were inserted into expression vectors.  
CC By coexpression of appropriate combinations of heavy and light  
CC chains, several humanised antibodies can be expressed. Coexpression  
CC of pHCW-1748RLA-gammaCI-dhfr and pHCW-1748RLA-KR-neo gives rise  
CC to the Pbl.3/humanised version A. Coexpression of pHCW-1747CH-  
CC gammaCI-neo and pHCW-1747-CL-KR-neo gives rise to the Pbl.3 chimera.  
CC These humanised antibodies selectively bind epitopes on P-selectin and  
CC block adhesion of leukocytes to the vascular endothelium. They may be  
CC used to treat inflammatory and thrombotic diseases and other

CC pathological conditions involving P-selectin and antibodies to it, esp.  
 CC acute lung injury and ischaemia reperfusion injury.  
 XX  
 SQ Sequence 106 AA:

Query Match 100.0%; Score 70; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNNGEC 13  
 |||||  
 DB 94 sspvtskfngrec 106

## RESULT 4

AAW37347  
 ID AAW37347 standard; Protein; 106 AA.

AC AAW37347;

DT 11-MAY-1998 (first entry)

XX Immunoglobulin C-kappa region.

DE Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;

KW gene amplification; immunotherapy; therapy; immunoglobulin;

XX C-kappa; constant region.

OS Homo sapiens.

XX WO9741244-A1.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US07039.

XX 06-DEC-1996; 96US-0761277.

XX 01-MAY-1996; 96US-0644664.

XX (GENI-) GENITOPE CORP.

XX Denney DW;

XX WPI: 1997-549743/50.

XX N-PSDB: AAT97190.

XX Multivalent vaccine to treat B cell lymphoma or leukaemia -

XX comprises at least 2 different recombinant variable regions of

XX immunoglobulin molecules derived from B cell lymphoma cells

XX Example 10; Page 127-128; 177pp; English.

XX This protein comprises an immunoglobulin (Ig) C-kappa region.

XX The invention provides a method for the production of tumour-

XX specific Ig derived from a B-cell lymphoma patient. In the novel

XX method, expression plasmids containing the patient's VH region(s)

XX joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)

XX sequence and expression plasmids containing the patient's VL

XX region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2

XX (see AAT97191) sequence are cotransfected along with a selectable and

XX amplified marker into a cell line (e.g. BW5147.G.1.4), and

XX transfected cells are then subjected to selection and amplification.

XX The method permits the production of a multivalent vaccine which

XX reflects the degree of somatic variation found within the patient's

XX tumour. These novel multivalent vaccines provide superior vaccines

XX for the treatment of B-cell lymphoma.

XX Sequence 106 AA;

XX Query Match 100.0%; Score 70; DB 18; Length 106;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNNGEC 13  
 |||||  
 DB 94 sspvtskfngrec 106

## RESULT 5

AAW59622  
 ID AAW59622 standard; Protein; 106 AA.

AC AAW59622;

DT 12-OCT-1998 (first entry)

XX Anti-RSV F protein Hu19 MAB light chain constant region.

DE Monoclonal antibody; human; Hu19C; Hu19D; engineered antibody; RSV;

KW respiratory syncytial virus; complementarity determining region;

XX CDR; infection; immunotherapy; therapy; diagnosis.

OS Homo sapiens.

XX WO9819704-A1.

XX 14-MAY-1998.

XX 23-OCT-1997; 97WO-US19203.

XX 01-NOV-1996; 96US-0030149.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Deen KC, Dillon SB, Porter TG, Sweet RW;

XX WPI: 1998-286600/25.

XX Monoclonal antibodies reactive with Respiratory Syncytial Virus -

XX useful for detection, prevention and treatment of RSV infections

XX Disclosure; Fig 3; 109pp; English.

XX This is the amino acid sequence of the light chain constant region

XX (C kappa) of constructs 19C and 19D of novel human monoclonal

XX antibodies (MAbs) reactive with the fusion (F) protein of

XX respiratory syncytial virus (RSV). Hu19A, Hu19B, Hu19C and Hu19D

XX MAbs are claimed. These are reshaped human antibodies comprising a

XX heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18); and

XX a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).

XX Such engineered antibodies are neutralising; they inhibit virus

XX growth in vitro and in vivo in animal models of RSV infection.

XX They can be used in the detection, prevention and passive

XX immunotherapy of RSV infection. Nucleic acids encoding the human

XX COS, CHO, myeloma) are provided.

XX Sequence 106 AA;

XX Query Match 100.0%; Score 70; DB 19; Length 106;

XX Best Local Similarity 100.0%; Pred. No. 4.1e-05;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 SSPVTKSFNNGEC 13

XX |||||

XX DB 94 sspvtskfngrec 106

XX RESULT 6

XX AAW48649

XX ID AAW48649 standard; Protein; 106 AA.

XX AC AAW48649;

```

XX 04-AUG-1998 (first entry)
DT Constant region of hmAb425 light chain.
XX
DE Antibody-cytokine fusion protein: tricistronic vector:
XX TNF alpha; IL-2; IRES; internal ribosome entry site.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9811241-A1.
XX
PD 19-MAR-1998.
XX
PF 02-SEP-1997; 97WO-EP04765.
XX
PR 30-SEP-1996; 96EP-0115635.
PR 16-SEP-1996; 96EP-0114820.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Bruemmer W, Burge C, Dunker R, Hauser H, Mielke C;
PI Rieke E, Von Hoeegen I, Welge T;
XX
DR WPI: 1998-207400/18.
DR N-PSDB: AAV18096.
XX
PT Oligo:cistronic expression vector - useful for production of, e.g.
PT MAb425/TNF- $\alpha$  or MAb425/IL-2 antibody fusion protein
XX
PS Disclosure: Fig 15; 89pp; English.
XX
CC The present sequence represents the constant region of the humanized
CC monoclonal antibody 425 (hmAb425) light chain. The hmAb425 has
CC specificity for the human EGF receptor. The invention claims for a
CC new pmcIDMAP tricistronic vector (AAV18096) for the expression of an
CC antibody-cytokine fusion protein, hmAb425-TNF alpha. hmAb425-TNF
CC alpha comprises of the TNF alpha, fused to the C-terminus of the heavy
CC chain of the hmAb425. The TNF alpha sequence can be substituted by the
CC IL-2 sequence. The vector also contains a strong promoter/enhancer
CC unit, a selection marker gene and at least two poliovirus derived
CC internal ribosomal entry site (IRES) sequences. The vector can be
CC expressed in mammalian host cells for the production of heteromeric
CC fusion proteins. This expression system is claimed to produce the
CC heteromeric proteins in high yields.
CC
XX Sequence 106 AA:
SQ

```

Query Match 100.0%; Score 70; DB 19; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 SSPVTKSFNRGEC 13
DB 94 SSPVTKSFNRGEC 106

```

RESULT 7  
 AAB04072  
 ID AAB04072 standard; Protein: 106 AA.  
 AC AAB04072;  
 XX  
 DT 11-APR-2001 (first entry)  
 XX  
 DE Interleukin receptor subunit::human kappa light chain fusion protein.  
 XX  
 KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;  
 KW binding; detection; modulation; recombinant cell;  
 KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;  
 KW immune system; blood; bone; inflammatory response; inflammation;

```

KW spleen; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2000068381-A1.
XX
PD 16-NOV-2000.
XX
PF 11-MAY-2000; 2000WO-US12924.
XX
PR 11-MAY-1999; 99US-0309861.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX
DR WPI: 2001-016096/02.
DR N-PSDB: AAA54474.
XX
PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
PT that stimulate proliferation or development of haematopoietic,
PT lymphoid and myeloid cells
XX
PS Example 17; Page 122-123; 134pp; English.
XX
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. These cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. A vector expressing a
CC secreted human zcytor 10 heterodimer is constructed. In this
CC construct the extracellular cytokine binding domain of zcytor 10
CC is fused to the heavy chain of IgG gamma and the extracellular
CC portion of the heteromeric cytokine receptor subunit (an
CC interleukin receptor subunit) is fused to human kappa light
CC chain (See GENESDB record AAA54474). The two sequences are fused
CC together using two primers (AAA54475, AAA54476).
CC
XX Sequence 106 AA:
SQ

```

Query Match 100.0%; Score 70; DB 22; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 SSPVTKSFNRGEC 13
DB 94 SSPVTKSFNRGEC 106

```

RESULT 8  
 AAM40578  
 ID AAM40578 standard; Protein: 107 AA.  
 AC AAM40578;  
 XX  
 DT 21-JUL-1998 (first entry)  
 XX  
 DE Human kappa CL domain protein fragment.

KM Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;  
KM disorder; salvage receptor binding epitope; cell adherence interaction;  
KM lymphocyte; T cell inflammatory response.  
XX  
OS Homo sapiens.  
XX  
PN US5739277-A.  
XX  
PD 14-APR-1998.  
XX  
PF 14-APR-1995; 95US-0422101.  
XX  
PR 14-APR-1995; 95US-0422101.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Presta LG, Smedecor BR;  
XX  
DR WPI: 1998-250490/22.  
XX  
PT Polypeptide(s) that are not Fc fragments and have an increased  
XX half-life - are useful for the treatment of LFA-1 mediated disorders  
XX  
PS Disclosure; Fig 2; 38pp; English.  
XX  
CC This protein fragment is derived from a human immunoglobulin kappa CL  
CC domain and is used to describe a novel method to produce polypeptides  
CC which contain an epitope from the Fc region of an IgG molecule and a  
CC mutated salvage receptor binding epitope. They are useful for the  
CC treatment of LFA-1 mediated disorders. These are conditions caused by  
CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,  
CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence  
CC in the polypeptides means that they have increased in vivo circulatory  
CC half-lives when compared to normal Fc regions of IgG molecules.  
XX  
SQ Sequence 107 AA:  
XX  
Query Match 100.0%; Score 70; DB 19; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SSPVTKSFNRGEC 13  
DB 95 ssptkspfngc 107  
XX  
RESULT 9  
AAVS0152  
ID AAVS0152 standard; Protein; 107 AA.  
XX  
AC AAVS0152;  
XX  
DT 31-JAN-2000 (first entry)  
XX  
DE Human kappa light chain constant region.  
XX  
KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;  
XX humanisation; complementarity determining region; CDR; CDR grafting;  
XX reshaped; reactive stroma; fibroblast; epithelial cancer;  
XX diagnosis; immune response; framework sequence; constant region;  
XX variable region; productibility; treatment; cancer; colorectal; lung;  
XX breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;  
XX detection; wound healing; skin inflammation; tumour; immunogenicity;  
XX light chain.  
XX  
OS Homo sapiens.  
XX  
PN EP953639-A1.  
XX  
PD 03-NOV-1999.  
XX  
PF 30-APR-1998; 98EP-0107925.

XX  
PR 30-APR-1998; 98EP-0107925.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
PI Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;  
XX Rettig WJ;  
XX  
DR WPI: 1999-621833/54.  
XX  
DR N-PSDB: AA232777.  
XX  
PT New antibody protein, useful for treating cancer and for imaging  
XX presence of activated stromal fibroblasts in healing wound or inflamed  
XX skin -  
XX  
PS Disclosure; Fig 20; 143pp; English.  
XX  
CC This sequence represents a human kappa light chain, the cDNA of which  
CC was used in the construction of a nucleotide encoding the light chain  
CC of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number  
CC HB 8269) is a murine monoclonal antibody against fibroblast  
CC activation protein alpha (FAP). FAP is a cell surface molecule  
CC of reactive stromal fibroblasts, and its induction is a highly  
CC consistent molecular trait of the reactive stroma of many types of  
CC epithelial cancer. Although F19 may be useful in vitro, e.g., for  
CC diagnosis, its applications for in vivo use in humans are problematic  
CC as it elicits a human anti-mouse response which reduces the efficacy of  
CC the antibody in patients and impairs continued administration. The novel  
CC human reshaped F19 was humanised by grafting the murine complementarity  
CC determining regions (CDRs) of F19 onto human variable region framework  
CC sequences, and then joining these "reshaped human" variable regions to  
CC human constant regions. These modifications also result in the improved  
CC producibility in eukaryotic cell culture systems as compared to a  
CC chimeric antibody having the entire variable regions of F19 joined to  
CC human constant regions. The human reshaped F19 antibody has low  
CC immunogenicity for humans and is useful for treating cancers e.g.,  
CC colorectal cancers, non-small cell lung cancers, breast cancers, head  
CC and neck cancers, ovarian cancers, lung cancers, bladder cancers,  
CC pancreatic cancers and metastatic cancers. It is also useful for the  
CC detection of activated stromal fibroblasts in a healing wound, inflamed  
CC skin or a tumour in a human patient.  
XX  
SQ Sequence 107 AA:  
XX  
Query Match 100.0%; Score 70; DB 20; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SSPVTKSFNRGEC 13  
DB 95 ssptkspfngc 107  
XX  
RESULT 10  
AAV08745  
ID AAV08745 standard; Protein; 107 AA.  
XX  
AC AAV08745;  
XX  
DT 10-AUG-1999 (first entry)  
XX  
DE Human Kappa-CL domain.  
XX  
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;  
XX IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;  
XX cerebroprotective; cerebral artery obstruction; blood flow; infarct;  
XX CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;  
XX antibody.  
XX  
OS Homo sapiens.  
XX  
PN US5914112-A.

XX 22-JUN-1999.  
PD  
XX  
XX 22-JAN-1997; 97US-0788800.  
PF  
XX 23-JAN-1996; 96US-0093038.  
PR 22-JAN-1997; 97US-0788800.  
PR  
XX (GETH ) GENENTECH INC.  
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.  
PI Bednar MM, Gross CE, Thomas GR;  
XX WPI: 1999-370483/31.  
DR  
XX Anti-CD18 antibodies in stroke  
PT  
XX  
PS Disclosure: Fig 4A-B; 25pp; English.  
XX  
XX This invention describes a method for improving the clinical outcome in  
CC focal ischaemic stroke by administering novel anti-CD18 antibody which  
CC has cerebroprotective properties. The invention particularly describes a  
CC method of treating focal ischaemic stroke caused by the obstruction of a  
CC main cerebral artery which comprises administering an anti-CD18 antibody  
CC to increase the blood flow or reduce the infarct size, where: (1) the  
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces  
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the  
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the  
CC antibody dissociates CD18/CD18 complex. This sequence represents the  
CC human Kappa-CL domain which is used to illustrate the method of the  
CC invention.  
CC  
XX Sequence 107 AA;  
SQ

Query Match 100.0%; Score 70; DB 20; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
IIIIIIIIIIIIII  
Db 95 ssptkstrngc 107

RESULT 11  
AAW92425  
ID AAW92425 standard; peptide: 107 AA.  
XX  
XX AAW92425;  
AC  
XX 23-APR-1999 (first entry)  
DT  
XX  
XX Human Kappa protein CL domain.  
DE  
XX  
XX Antibody; salvage receptor binding epitope: Fab: F(ab')<sub>2</sub>; immunoglobulin;  
KW CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; IgG;  
KW kappa protein; renal clearance rate; circulatory half-life.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US5869046-A.  
PN  
XX 09-FEB-1999.  
PD  
XX 14-APR-1995; 95US-0422092.  
PF  
XX 14-APR-1995; 95US-0422092.  
PR  
XX 14-APR-1995; 95US-0422092.  
PS  
XX (GETH ) GENENTECH INC.  
PA  
XX Presta LG, Snedecor BR;  
PI  
XX WPI: 1999-152694/13.  
DR

XX Production of antibody fragments with reduced renal clearance - by  
PT introducing salvage receptor binding epitope into CH1 or CL region  
XX  
XX  
PS Disclosure: Column 55-58; 38pp; English.  
XX  
XX This invention describes a method for preparing a variant Fab or F(ab')<sub>2</sub>  
CC polypeptide having increased half-life in vivo, where the polypeptide  
CC contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is  
CC cleared from the kidneys and does not contain an IgG Fc region. The  
CC method involves altering the polypeptide within the CH1 or CL region to  
CC incorporate a salvage receptor binding epitope taken from two loops of  
CC a CH2 domain of an IgG Fc region. The polypeptides have a reduced renal  
CC clearance rate and an increased circulatory half-life. This sequence  
CC represents a human kappa protein CL domain used in the method of the  
CC invention.  
CC  
XX Sequence 107 AA;  
SQ

Query Match 100.0%; Score 70; DB 20; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
IIIIIIIIIIIIII  
Db 95 ssptkstrngc 107

RESULT 12  
AAB27000  
ID AAB27000 standard; Protein: 107 AA.  
XX  
XX AAB27000;  
AC  
XX 25-JAN-2001 (first entry)  
DT  
XX  
XX Human kappa CL domain.  
DE  
XX  
XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;  
KW mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;  
KW psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;  
KW inflammation; vaccine.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX US6121022-A.  
PN  
XX 19-SEP-2000.  
PD  
XX 14-APR-1995; 95US-0422112.  
PF  
XX 14-APR-1995; 95US-0422112.  
PR  
XX 14-APR-1995; 95US-0422112.  
PS  
XX (GETH ) GENENTECH INC.  
PA  
XX Presta LG, Snedecor BR;  
PI  
XX WPI: 2000-610925/58.  
DR  
XX  
XX New nucleic acid encoding new modified polypeptides with increased  
PT circulatory half-life useful for preventing/treating LFA-1 mediated  
PT disorders, e.g. reducing inflammatory responses or inducing tolerance  
PT to immunostimulants  
XX  
XX  
PS Disclosure: Fig 2; 38pp; English.  
XX  
XX The present sequence was used in a method for improving the in vivo  
CC half-life of polypeptides. The polypeptides comprise an Ig constant  
CC domain or an Ig-like constant domain, and a salvage receptor binding  
CC epitope within the Ig or Ig-like domain. The salvage receptor epitope is  
CC taken from two loops of the CH2 domain of an Fc region of an Ig molecule.  
CC The modified polypeptides are useful for preventing or treating



CC LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis,  
 CC allergic conditions (e.g. eczema); antigen-antibody complex mediated  
 CC diseases, B-cell lymphomas. They are also useful for wound repair,  
 CC reducing inflammatory responses and inducing tolerance to  
 CC immunostimulants. They may also be used in diagnostic assays. The nucleic  
 CC acids and modified polypeptides are useful for the passive immunisation  
 CC of patients, as well as for affinity purification of an antigen from  
 CC recombinant cell culture or natural sources.  
 CC  
 XX Sequence 107 AA:

Query Match 100.0%; Score 70; DB 21; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
 |||||  
 DB 95 sspvtskfngrec 107

RESULT 13  
 AAB62265  
 ID AAB62265 standard; Protein; 107 AA.  
 XX  
 AC AAB62265;  
 XX  
 DT 11-JUN-2001 (first entry)  
 XX  
 DE Light chain construct A31A amino acid fragment.  
 XX  
 KM Fusion protein; cell surface antigen; cancer; monoclonal antibody;  
 KM light chain construct; carcinogenic.  
 XX  
 OS Mammalia.  
 XX  
 PN WO200119842-A1.  
 XX  
 PD 22-MAR-2001.  
 XX  
 PF 18-SEP-2000; 2000WO-US25558.  
 XX  
 PR 17-SEP-1999; 99US-0399079.  
 XX  
 PA (GENZ ) GENZYME TRANSGENICS CORP.  
 XX  
 PI Pollock D, Meade HM, Bosslet K;  
 XX  
 DR MPI: 2001-257871/26.  
 DR N-PSDB; AAF57571.  
 XX

PT New fusion protein, useful for killing diseased cells e.g. cancer  
 PT cells, comprises fused first and second units, such that the protein  
 PT assembles into complex which optimizes activity of multimeric form of  
 PT second unit -  
 XX  
 PS Example 1; Fig 1B: 88pp; English.  
 XX  
 CC The invention relates to a fusion protein (I) comprising a first member  
 CC fused to a second member, where the first and second members are chosen  
 CC such that (I) assembles into a complex having a number of subunits which  
 CC optimizes activity of the multimeric form of the second member. (I) is  
 CC useful for selectively killing an aberrant or diseased cell which  
 CC expresses a target antigen on its surface, e.g., a cancer cell expressing  
 CC a cell surface antigen. (I) is also useful for detecting in vitro or in  
 CC vivo the presence of target antigen in a sample, e.g., for diagnosing a  
 CC disease, by contacting a sample or a control sample that allows  
 CC interaction of (I) which is labeled, and detecting formation of a  
 CC complex. (I) is also useful for selectively directing (e.g., localizing)  
 CC the second unit of (I) to the vicinity of an undesirable cell. The  
 CC present sequence represents a fragment of a light chain construct A31A  
 CC that was generated using the light chain sequence from a humanised Mab  
 CC against carcinoembryonic antigen (431).

XX  
 SQ Sequence 107 AA:

Query Match 100.0%; Score 70; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
 |||||  
 DB 95 sspvtskfngrec 107

RESULT 14  
 AAW70802  
 ID AAW70802 standard; Protein; 108 AA.  
 XX  
 AC AAW70802;  
 XX  
 DT 03-FEB-1999 (first entry)  
 XX  
 DE Amino acid sequence of the kappa domain.  
 XX  
 KM gp130; cytokine antagonist; interleukin; gamma-interferon;  
 KM granulocyte macrophage colony-stimulating factor; J peptide;  
 KM transforming growth factor-beta.  
 XX  
 OS Synthetic.  
 XX  
 PN US5844099-A.  
 XX  
 PD 01-DEC-1998.  
 XX  
 PF 27-NOV-1995; 95US-0563105.  
 XX  
 PR 27-NOV-1995; 95US-0563105.  
 PR 20-OCT-1993; 93US-0140222.  
 XX  
 PA (REGG-) REGENERON PHARM INC.  
 XX  
 PI Economides A, Stahl N, Yancopoulos GD;  
 XX  
 DR MPI: 1999-044669/04.  
 XX  
 PT Cytokine antagonists - comprising extracellular domains of  
 PT specificity-determining and signal-transducing components of  
 PT cytokine receptor  
 XX  
 PS Example 4; Fig 13; 46pp; English.  
 XX  
 CC The present sequence represents the amino acid sequence of  
 CC kappa domain. The protein is used in the course of the invention.  
 CC The specification describes cytokine antagonists comprising only the  
 CC extracellular domain of the specificity-determining component of  
 CC the cytokine receptor and the extracellular domain of a  
 CC signal-transducing component of the cytokine receptor. The cytokine  
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),  
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),  
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The  
 CC antagonist is capable of binding the cytokine to form a nonfunctional  
 CC complex. The compounds have therapeutic activity as cytokine antagonists  
 CC and can also be used in assays for identifying novel agonists and  
 CC antagonists of cytokines.  
 XX

SQ Sequence 108 AA:

Query Match 100.0%; Score 70; DB 20; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
 |||||

Db 96 ssptkstrngec 108

RESULT 15  
AAV92191  
ID AAV92191 standard; protein; 108 AA.  
XX  
AC AAV92191;  
XX  
DT 01-AUG-2000 (first entry)  
XX  
DE Human IgG1 kappa domain.  
XX  
KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;  
XX cytosolic; immunomodulator; osteopathic.  
XX  
OS Synthetic.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..2  
FT /note= "Ser-gly bridge"  
FT Domain 3..107  
FT /label= kappa\_domain  
XX  
PN W0200018932-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 22-SEP-1999; 99WO-US22045.  
XX  
PR 25-SEP-1998; 98US-0101858.  
PR 19-MAY-1999; 99US-0313942.  
XX  
PA (REGG-) REGENERON PHARM INC.  
XX  
PI Stahl N, Yancopoulos GD;  
XX  
DR WPI; 2000-293165/25.  
XX  
PT Isolated nucleic acid molecule for treating cytokine-related diseases  
PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
PT to form a nonfunctional complex  
XX  
PS Example 4; Fig 13; 152pp; English.  
XX  
CC The invention concerns production of antagonists to any cytokine that  
CC utilizes an alpha specificity determining component, which when combined  
CC with the cytokine, binds to a first beta signal transducing component to  
CC form a non-functional intermediate which then binds to a second beta  
CC signal transducing component causing beta-receptor dimerization, the  
CC soluble alpha specificity determining component of the receptor  
CC (SR-alpha) and the extracellular domain of the first beta signal  
CC transducing component of the cytokine receptor (beta-1) are combined to  
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the  
CC cytokine by binding the cytokine to form a non-functional complex. The  
CC receptor components are shared by cytokines such as the CNTF (ciliary  
CC neurotrophic factor) family of cytokines. The invention provides the  
CC basis for the development of IL-6 antagonists, as they show that if, in  
CC the presence of a ligand, a non-functional intermediate complex,  
CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
CC component, can be formed, it will effectively block the action of the  
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
CC of the extracellular domains of the alpha specificity determining  
CC components of their receptors and the extracellular domain of gp130.  
CC The resultant heterodimers, function as high-affinity traps, rendering  
CC the cytokine inaccessible to form a signal transducing complex with the  
CC native membrane-bound forms of their receptor. The nucleic acids and  
CC polypeptides are useful for treating cytokine-related diseases or  
CC disorders such as osteoporosis and primary and secondary effects of  
CC cancer including multiple myeloma or cachexia.  
SQ Sequence 108 AA;

Query Match 100.0%; Score 70; DB 21; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SSPYTKSFNRGEC 13  
DB 96 ssptkstrngec 108

Search completed: January 4, 2002, 18:09:11  
Job time: 276 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:09:37 ; Search time 19.66 Seconds

(without alignments)  
14.880 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPYTKSFNRREC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/plodata/2/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/plodata/2/iaa/5A.COMB.pep:\*  
3: /cgn2\_6/plodata/2/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/plodata/2/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/plodata/2/iaa/PCFUS.COMB.pep:\*  
6: /cgn2\_6/plodata/2/iaa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	106	2	US-08-378-939-40
2	70	100.0	106	2	US-08-378-939-42
3	70	100.0	106	2	US-08-761-277A-49
4	70	100.0	106	3	US-08-444-644-26
5	70	100.0	107	1	US-08-422-101-8
6	70	100.0	107	1	US-08-422-091-8
7	70	100.0	107	2	US-08-422-092-8
8	70	100.0	107	2	US-08-788-800-5
9	70	100.0	107	3	US-08-422-093-8
10	70	100.0	107	3	US-08-422-112-8
11	70	100.0	143	1	US-08-236-311-10
12	70	100.0	143	3	US-08-437-918-10
13	70	100.0	213	3	US-08-630-820-6
14	70	100.0	213	3	US-08-397-411-12
15	70	100.0	214	1	US-08-425-763-1
16	70	100.0	214	1	US-08-253-877C-5
17	70	100.0	214	1	US-08-458-516-12
18	70	100.0	214	2	US-07-934-373C-24
19	70	100.0	214	2	US-07-934-373C-39
20	70	100.0	214	2	US-07-934-373C-40
21	70	100.0	214	2	US-08-480-753-6
22	70	100.0	214	2	US-08-452-164A-5
23	70	100.0	214	2	US-08-788-800-11
24	70	100.0	214	3	US-09-041-889-11
25	70	100.0	214	3	US-08-437-642B-24
26	70	100.0	214	3	US-08-437-642B-39
27	70	100.0	214	3	US-08-437-642B-40

#### ALIGNMENTS

28	70	100.0	214	3	US-08-811-757-1	Sequence 1, Appl
29	70	100.0	214	3	US-08-837-058-11	Sequence 11, Appl
30	70	100.0	214	3	US-09-097-309-2	Sequence 2, Appl
31	70	100.0	214	3	US-08-397-411-5	Sequence 2, Appl
32	70	100.0	214	4	US-09-097-171A-2	Sequence 2, Appl
33	70	100.0	214	4	US-09-249-230-1	Sequence 1, Appl
34	70	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appl
35	70	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appl
36	70	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appl
37	70	100.0	215	2	US-08-480-753-8	Sequence 8, Appl
38	70	100.0	218	2	US-08-887-352B-13	Sequence 13, Appl
39	70	100.0	218	2	US-08-887-352B-15	Sequence 15, Appl
40	70	100.0	218	2	US-08-887-352B-17	Sequence 17, Appl
41	70	100.0	218	2	US-08-887-352B-19	Sequence 19, Appl
42	70	100.0	218	2	US-08-887-352B-24	Sequence 24, Appl
43	70	100.0	218	3	US-08-466-151-9	Sequence 9, Appl
44	70	100.0	218	4	US-09-109-207C-13	Sequence 13, Appl
45	70	100.0	218	4	US-09-109-207C-15	Sequence 15, Appl

RESULT 1  
US-08-378-939-40  
; Sequence 40, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROME, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEO ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-40

Query Match 100.0%; Score 70; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SSPYTKSFNRREC 13  
|||||

Db 94 SSPVTKSFNRGEC 106

## RESULT 2

US-08-378-939-42

Sequence 42, Application US/08378939

Patent No. 5876961

GENERAL INFORMATION:

APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST &amp; KURZ

STREET: 555 THIRTEENTH ST. N.W.

CITY: WASHINGTON

STATE: D. C.

COUNTRY: U.S.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,939

FILING DATE:

CLASSIFICATION: 439

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-939-42

Query Match 100.0%; Score 70; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVTKSFNRGEC 106

## RESULT 3

US-08-761-277A-49

Sequence 49, Application US/08761277A

Patent No. 5972334

GENERAL INFORMATION:

APPLICANT: Denney Jr., Dan W.

TITLE OF INVENTION: VACCINES For Treatment Of Lymphoma And

TITLE OF INVENTION: Leukemia

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen &amp; Cartoll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/761,277A

FILING DATE: 06-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/644,664

FILING DATE: 01-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: GENIHOPE-02406

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-761-277A-49

Query Match 100.0%; Score 70; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVTKSFNRGEC 106

## RESULT 4

US-08-444-644-26

Sequence 26, Application US/08444644

Patent No. 6015555

GENERAL INFORMATION:

APPLICANT: Friden, Phillip M.

TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC

TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

STREET: Two Millita Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,644

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,246

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/800,458

FILING DATE: 26-NOV-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCU/US90/05077

FILING DATE: 07-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/404,089

FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-444-644-26

Query Match 100.0%; Score 70; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
|||||  
Db 94 SSPVTKSFNRGEC 106

RESULT 5  
US-08-422-101-8  
Sequence 8, Application US/08422101  
Patent No. 5739277  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,101  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-101-8

Query Match 100.0%; Score 70; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
|||||  
Db 95 SSPVTKSFNRGEC 107

RESULT 6  
US-08-422-091-8  
Sequence 8, Application US/08422091  
Patent No. 5747035  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,091  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-091-8

Query Match 100.0%; Score 70; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
|||||  
Db 95 SSPVTKSFNRGEC 107

RESULT 7  
US-08-422-092-8  
Sequence 8, Application US/08422092  
Patent No. 5869046  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-092-8
;
Query Match          100.0%; Score 70; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
   |||||||
Db 95 SSPVTKSFNRGEC 107

RESULT 8
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 591412
;
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788.800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: linear
;
US-08-788-800-5
;
Query Match          100.0%; Score 70; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
   |||||||
Db 95 SSPVTKSFNRGEC 107

RESULT 9
US-08-422-093-8
; Sequence 8, Application US/08422093
; Patent No. 6096871
;
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.093
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-422-093-8
;
Query Match          100.0%; Score 70; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
   |||||||
Db 95 SSPVTKSFNRGEC 107
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RESULT 10

US-08-422-112-8  
 ; Sequence 8, Application US/08422112  
 ; Patent No. 6121022  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leonard Presta  
 ; APPLICANT: Brad Snedecor  
 ; TITLE OF INVENTION: Altered Polypeptides with Increased  
 ; TITLE OF INVENTION: Half-Life  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: palin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/422,112  
 ; FILING DATE: 14-APR-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Lee, Wendy M.  
 ; REGISTRATION NUMBER:  
 ; REFERENCE/DOCKET NUMBER: 932-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1994  
 ; TELEFAX: 415/952-9881  
 ; TELEEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-422-112-8

Query Match 100.0%; Score 70; DB 3; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
 |||  
 DB 95 SSPVTKSFNRGEC 107

RESULT 11

US-08-236-311-10  
 ; Sequence 10, Application US/08236311.  
 ; Patent No. 5565335  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Capon, Daniel J.  
 ; APPLICANT: Gregory, Timothy J.  
 ; TITLE OF INVENTION: Adheson Variants  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: palin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/236,311  
 ; FILING DATE: 02-MAY-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/936190  
 ; FILING DATE: 26-AUG-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/842777  
 ; FILING DATE: 18-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/250785  
 ; FILING DATE: 28-SEP-1988  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/104329  
 ; FILING DATE: 02-OCT-1987  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hasak, Janet E.  
 ; REGISTRATION NUMBER: 28,616  
 ; REFERENCE/DOCKET NUMBER: 444P1C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-1896  
 ; TELEFAX: 415/952-9881  
 ; TELEEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 143 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-236-311-10

Query Match 100.0%; Score 70; DB 1; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
 |||  
 DB 131 SSPVTKSFNRGEC 143

RESULT 12

US-08-457-918-10  
 ; Sequence 10, Application US/08457918  
 ; Patent No. 6117655  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Capon, Daniel J.  
 ; APPLICANT: Gregory, Timothy J.  
 ; TITLE OF INVENTION: Adheson Variants  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: palin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/457,918  
 ; FILING DATE: 1-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/236311  
 ; FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444P1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 143 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-457-918-10

Query Match 100.0%; Score 70; DB 3; Length 143;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 131 SSPVTKSFNRGEC 143

RESULT 13  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: Oppper, Martin  
APPLICANT: Bosslet, Klaus  
APPLICANT: CZECH, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-6

Query Match 100.0%; Score 70; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 201 SSPVTKSFNRGEC 213

RESULT 14  
US-08-397-411-12  
Sequence 12, Application US/08397411  
Patent No. 6126914  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Gingrich, Roger  
APPLICANT: Link, Brian  
APPLICANT: Tso, J. Yun  
TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,411  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/859,583  
FILING DATE: 27-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-004901  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2422  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-397-411-12

Query Match 100.0%; Score 70; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13



DB 201 SSPVTKSFNRGEC 213

RESULT 15

US-08-425-763-1

; Sequence 1, Application US/08425763

; Patent No. 5641870

; GENERAL INFORMATION:

; APPLICANT: Rinderknecht, Ernst H.

; APPLICANT: Zapata, Gerardo A.

; TITLE OF INVENTION: ANTIBODY PURIFICATION

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/425,763

; FILING DATE: 20-APR-1995

; CLASSIFICATION: 424

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 941

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELETYPE: 910/371-7168

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 214 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-425-763-1

Query Match 100.0%; Score 70; DB 1; Length 214;

Best Local Similarity 100.0%; Pred. No. 6.1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13

DB 202 SSPVTKSFNRGEC 214

Search completed: January 4, 2002, 18:09:37  
Job time: 252 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2002, 18:10:05 ; Search time 21.97 seconds  
(without alignments)  
45.074 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPVTKSFNRGEC 13

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : PIR68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	70	100.0	99	A37927	Ig kappa chain C r
2	70	100.0	106	K3HU	Ig kappa chain C r
3	70	100.0	135	S52059	JC-kappa protein -
4	70	100.0	215	JEO244	Ig kappa chain NTG
5	70	100.0	215	JEO242	Ig kappa chain NTG
6	70	100.0	215	JEO243	Ig kappa chain NTG
7	70	100.0	215	JEO241	Ig kappa chain NTG
8	61	87.1	215	A23746	Ig kappa chain V-1
9	61	87.1	217	S42772	Ig kappa chain V-1
10	61	87.1	218	S68241	Ig kappa chain V r
11	61	87.1	219	S38865	Ig kappa chain - m
12	59	84.3	106	K1RTB	Ig kappa chain C r
13	59	84.3	106	K1RTA	Ig kappa chain C r
14	59	84.3	240	S06084	Ig kappa chain pre
15	55	78.6	106	K1MS	Ig kappa chain C r
16	55	78.6	126	I54782	gene Pvt-1a/Ig-CK
17	55	78.6	218	JC5810	monoclonal antibody
18	55	78.6	219	PC4203	Ig kappa chain (mo
19	55	78.6	219	S16112	Ig kappa chain V r
20	55	78.6	219	S52028	Ig kappa chain - m
21	55	78.6	220	A31790	Ig kappa chain V r
22	55	78.6	225	S37484	Ig kappa chain - m
23	55	78.6	225	J10029	Ig kappa chain pre
24	55	78.6	234	S14237	Ig kappa chain pre
25	55	78.6	234	S01320	Ig kappa chain pre
26	55	78.6	235	S25058	Ig kappa chain - m
27	54	77.1	106	K4RBS	Ig kappa chain - C
28	54	77.1	106	G20907	Ig kappa-B4 chain
29	47	67.1	178	PT0219	Ig kappa chain V-C

30	46	65.7	238	2	A49633	Ig lambda-like cha
31	45	64.3	229	2	A20969	Ig kappa chain pre
32	44	62.9	103	1	K4RB	Ig kappa-B4 chain
33	43	61.4	100	2	S29569	Ig light chain C r
34	43	61.4	107	2	S29572	Ig light chain - A
35	43	61.4	131	2	S29573	Ig light chain - A
36	43	61.4	197	2	S29574	Ig light chain - A
37	42	60.0	104	1	K9RR	Ig kappa-B9 chain
38	42	60.0	121	2	S19486	hypothetical prote
39	41	58.6	104	2	F53275	Ig kappa-1 chain C
40	40	57.9	772	2	S02665	gelsolin precursor
41	40	57.1	548	2	T18761	hypothetical prote
42	42	55.7	85	2	S29576	Ig light chain - r
43	39	55.7	104	1	K5RRV	Ig kappa chain C r
44	39	55.7	167	2	S29579	Ig light chain - r
45	39	55.7	228	2	S29575	Ig light chain - r

#### ALIGNMENTS

RESULT 1  
A37927  
Ig kappa chain C region (allotype Inv(1.2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: A37927  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
Db 87 SSPVTKSFNRGEC 99

RESULT 2  
K3HU  
Ig kappa chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: B90562; A91651; A90806; A94417; A91639; A94244; B37927; A02116;  
R:cottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequ  
A:Reference number: A90562; MUID:71064023  
A:Accession: B90562  
A:Molecule type: protein  
A:Residues: 1-106 <GOT>  
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul  
A:Contents: annotation; Eu, disulfide bonds  
R:Buter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ.  
A:Reference number: A91651; MUID:72188439

A:Contents: Bence Jones protein T1  
A:Accession: A91631  
A:Molecule type: protein  
A:Residues: 1-106 <SUT>  
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Malzel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv  
A:Reference number: A90806; MUID:81042304  
A:Accession: A90806  
A:Molecule type: DNA  
A:Residues: 1-106 <HE>  
A:Cross-references: GB:00241; NID:933140; PIDN:CA23823.1; PID:91335148  
A:Note: the sequence was determined from the germ-line gene  
R:Hiltschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponslingl, H.; Steinmetz-Kayne,  
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,  
A:Reference number: A94417  
A:Contents: Bence Jones protein Roy  
A:Accession: A94417  
A:Molecule type: protein  
A:Residues: 1-44, 'A', 46-56, 'Q', 58-82, 'L', 84-106 <HIL>  
A:Note: this sequence has the inv (1.2) allotypic marker, 45-Ala and 83-Leu  
R:Hiltschmann, N.  
Hope-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A:Title: Die volstandige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (Kappa-Typ).  
A:Reference number: A91639; MUID:68242255  
A:Contents: Bence Jones protein Cum  
A:Accession: A91639  
A:Molecule type: protein  
A:Residues: 1-56, 'Q', 58-106 <H12>  
R:Titani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <RT>  
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507  
A:Contents: Waldenstrom's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13, 'N', 15-106 <KOH>  
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Note: allozyme Inv(3)  
R:Steiner, V.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-references: GDB:120086; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kap  
hain disulfide bonds: in some cases, such as IGA and IGM, the subunits associate into 16  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMW>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 100.0%; Score 70; DB 1; Length 106;

Best Local Similarity 100.0%; Pred. No. 3.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 94 SSPVTKSFNRGEC 106

## RESULT 3

S52059  
JC-Kappa protein - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Sep-2000  
C:Accession: S52059  
R:Frances, V.; Pandreau-Garcia, D.; Gurec, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland,  
EMBO J. 13, 5937-5943, 1994  
A:Title: A surrogate 15 kDa JC-Kappa protein is expressed in combination with mu heav  
A:Reference number: S52059; MUID:95112804  
A:Accession: S52059  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <FRA>  
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 100.0%; Score 70; DB 2; Length 135;  
Best Local Similarity 100.0%; Pred. No. 4.6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 123 SSPVTKSFNRGEC 135

## RESULT 4

JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazl, H.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <AL1>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 70; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 203 SSPVTKSFNRGEC 215

## RESULT 5

JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <AL1>

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 203 SSPVTKSFNRGEC 215

RESULT 6

JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243

R:Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (YKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALIT>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 7.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 203 SSPVTKSFNRGEC 215

RESULT 7

JE0241  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0241

R:Alim, M.A.; Yamaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mu]  
A:Reference number: JE0241  
A:Accession: JE0241  
A:Molecule type: protein  
A:Residues: 1-216 <ALIT>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 70; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 204 SSPVTKSFNRGEC 216

RESULT 8

A23746  
Ig kappa chain V-III (KAV cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C>Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991

A>Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immun  
A:Reference number: A23746; MUID:91131575

A:Accession: A23746  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 61; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGE 12  
|||||  
Db 203 SSPVTKSFNRGE 214

RESULT 9

S42772  
Ig kappa chain - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C:Accession: S42772  
R:Schellekens, G.A.  
submitted to the EMBL Data Library, November 1993  
A:Reference number: S42772  
A:Accession: S42772  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SCH>

A:Cross-references: EMBL:X75536; NID:g414143; PID:CA53226.1; PID:g414144  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 87.1%; Score 61; DB 2; Length 217;  
Best Local Similarity 76.9%; Pred. No. 0.00041;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
|||||  
Db 205 TSPVTKSFNRGEC 217

RESULT 10

S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C>Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C:Accession: S68241  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,  
submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porph  
A:Reference number: S68241  
A:Accession: S68241  
A:Molecule type: mRNA  
A:Residues: 1-218 <TAK>  
A:Cross-references: EMBL:D29670; NID:g473962; PID:BA06141.1; PID:g473963  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,  
FEBS Lett. 375, 273-276, 1995  
A>Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr  
A:Accession: S68214  
A:Reference number: S68214; MUID:96085223  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 'N', 3-212 <TAM>  
A:Cross-references: EMBL:D29670  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 87.1%; Score 61; DB 2; Length 218;  
Best Local Similarity 76.9%; Pred. No. 0.00041;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
DB 206 TSPIVKSFNREGC 218

RESULT 11

Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-2001  
C:Accession: S38865  
R:Klpp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A:Description: Combination of a defined specificity and desired isotype by cloning of an  
A:Reference number: S38864  
A:Accession: S38865  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <KIP>  
A:Cross-references: EMBL:227396; NID:9416538; PIDN:CAA81787.1; PID:9416539  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 87.1%; Score 61; DB 2; Length 219;  
Best Local Similarity 76.9%; Pred. No. 0.00041;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
DB 207 TSPIVKSFNREGC 219

RESULT 12

KIRTB  
Ig kappa chain C region (allele b) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 28-May-1999  
C:Accession: A93901; A92807; A02117  
R:Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the Ig  
A:Reference number: A93901; MUID:82082587  
A:Accession: A93901  
A:Molecule type: DNA  
A:Residues: 1-106 <SHE>  
A:Cross-references: GB:J01241; GB:J00745; GB:J02574; GB:J02575; NID:957849; PIDN:CAA2455  
A:Experimental source: strain LOU  
R:Starace, V.; Querinjean, P.  
J. Immunol. 115, 59-62, 1975  
A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation  
A:Reference number: A92807; MUID:75212228  
A:Contents: Bence Jones protein S211  
A:Accession: A92807  
A:Molecule type: protein  
A:Residues: 1, 'N', 'K', '31-47', '49-78', '80-86', '88-98', '99', '101-106 <STA>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:19-88/Domain: Immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status predicted  
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 84.3%; Score 59; DB 1; Length 106;

Best Local Similarity 84.6%; Pred. No. 0.00046;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
DB 94 SSPVKSFNREGC 106

RESULT 13

KIRTA  
Ig kappa chain C region (allele a) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Aug-1982 #sequence\_revision 10-Sep-1982 #text\_change 22-Jun-1999  
C:Accession: A02118  
R:Sheppard, H.W.; Gutman, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981  
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the  
A:Reference number: A93901; MUID:82082587  
A:Accession: A02118  
A:Molecule type: DNA  
A:Residues: 1-106 <SHE>  
A:Cross-references: GB:J02574; GB:J00745; NID:9204820; PIDN:AAA1411.1; PID:9204821  
A:Experimental source: strain DA  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status predicted  
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 84.3%; Score 59; DB 1; Length 106;  
Best Local Similarity 84.6%; Pred. No. 0.00046;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
DB 94 SSPVKSFNREGC 106

RESULT 14

S06084  
Ig kappa chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S06084  
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A:Title: Nucleotide sequence of Ig-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c  
A:Reference number: S06084; MUID:90016888.  
A:Accession: S06084  
A:Molecule type: mRNA  
A:Residues: 1-240 <CRO>  
A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-240/Product: Ig kappa chain #status predicted <ANT>  
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 59; DB 2; Length 240;  
Best Local Similarity 84.6%; Pred. No. 0.0011;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13  
DB 228 SSPVKSFNREGC 240

RESULT 15

KIMS

Ig kappa chain C region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1980 #sequence\_revision 17-Dec-1982 #text\_change 16-Aug-1996  
C:Accession: B90262; A90778; B93736; A92322; A93748; A02119  
R:Swastil, J.; Milstein, C.  
Biochem. J. 128, 427-444, 1972  
A:Title: The complete amino acid sequence of a mouse kappa light chain.  
A:Reference number: A90262; MUID:73053310  
A:Contents: myeloma protein MOPC 21  
A:Accession: B90262  
A:Molecule type: Protein  
A:Residues: 1-52, BSRZMB, 60-106 <SVA>  
R:Swastil, J.; Milstein, C.  
Biochem. J. 126, 837-850, 1972  
A:Title: The disulphide bridges of a mouse immunoglobulin G1 protein.  
A:Reference number: A90259; MUID:7300889  
A:Contents: annotation: MOPC 21, disulfide bonds  
A:Note: Cys-106 is involved in a light-heavy chain bond  
R:Hamlyn, P.H.; Brownlee, G.G.; Cheng, C.C.; Galt, M.J.; Milstein, C.  
Cell 15, 1067-1075, 1978  
A:Title: Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA  
A:Reference number: A90778; MUID:79084137  
A:Accession: A90778  
A:Molecule type: mRNA  
A:Residues: 1-106 <HAM>  
R:Hamlyn, P.H.; Galt, M.J.; Milstein, C.  
Nucleic Acids Res. 9, 4485-4494, 1981  
A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideo  
A:Reference number: A93736; MUID:82059477  
A:Contents: MOPC 21  
A:Accession: B93736  
A:Molecule type: mRNA  
A:Residues: 1-106 <HA2>  
R:Max, E.E.; Maizel Jr., J.V.; Leder, P.  
J. Biol. Chem. 256, 5116-5120, 1981  
A:Title: The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa  
A:Reference number: A92322; MUID:81191915  
A:Accession: A92322  
A:Molecule type: DNA  
A:Residues: 1-106 <MAX>  
A:Note: The sequence was determined from the germline gene  
R:Altenburger, W.; Neumaier, P.S.; Steinmetz, M.; Zachau, H.G.  
Nucleic Acids Res. 9, 971-981, 1981  
A:Title: DNA sequence of the constant gene region of the mouse immunoglobulin kappa chain  
A:Reference number: A93748; MUID:81198849  
A:Accession: A93748  
A:Molecule type: DNA  
A:Residues: 1-106 <ALT>  
A:Note: The sequence was determined from the germline gene  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two heavy (lambda) chains. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin C region, immunoglobulin homology  
C:Keywords: heterotetramer  
F:26-86/Disulfide bonds: #status experimental

Query Match 78.6%; Score 55; DB 1; Length 106;  
Best Local Similarity 69.2%; Pred. No. 0.0027;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13  
:||| ||| ||  
DB 94 TSPIVKSFNRNEC 106

Search completed: January 4, 2002, 18:10:05  
Job time: 225 sec

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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:14:37 ; Search time 15.29 Seconds  
(without alignments)  
31.173 Million cell updates/sec

Title: US-09-875-221A-113

Perfect score: 70

Sequence: 1 SSPVTKSFNNGEC 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	106	1 KAC_HUMAN	P01834 homo sapien
2	59	84.3	106	1 KACA_RAT	P01836 rattus norv
3	59	84.3	106	1 KACB_RAT	P01835 rattus norv
4	55	78.6	106	1 KAC_MOUSE	P01837 mus musculu
5	54	77.1	106	1 KACB_RABIT	P01839 oryctolagus
6	44	62.9	103	1 KACA_RABIT	P01840 oryctolagus
7	42	60.0	104	1 KAC9_RABIT	P01838 oryctolagus
8	42	60.0	121	1 YCWL_YEAST	P25642 saccharomyc
9	40.5	57.9	722	1 GELS_PIG	P20305 sus scrofa
10	39	55.7	104	1 KAC6_RABIT	P03984 oryctolagus
11	38	54.3	657	1 MRB_DROME	P04197 drosophila
12	37	52.9	455	1 MURE_BUCAL	P57315 buchneria ap
13	37	52.9	895	1 YAS4_METUA	Q58454 methanococc
14	36	51.4	177	1 CHR1_BOMMO	P13532 bombyx mori
15	36	51.4	354	1 MTD2_HERAV	P25265 herpetosiph
16	36	51.4	637	1 RES1_SCHRO	P33520 schizosacch
17	36	51.4	715	1 ADSV_MOUSE	Q60604 mus musculu
18	36	51.4	1057	1 RPOC_STAAU	P47770 staphylococ
19	36	51.4	1444	1 RRLP_RDVA	Q02119 rice dwarf
20	36	51.4	1444	1 RRLP_RDVA	Q02119 rice dwarf
21	35.5	50.7	730	1 GELS_HORSE	Q28372 equus caball
22	35.5	50.7	782	1 GELS_HORSE	Q28372 equus caball
23	35	50.0	59	1 YDBF_SCHRO	P06396 homo sapien
24	35	50.0	73	1 NXL1_KACAN	O10365 schizosacch
25	35	50.0	392	1 DCAM_LEBIN	P01385 acanthophis
26	35	50.0	492	1 SECV_CVAPA	Q9n9a0 leishmania
27	35	50.0	598	1 BCCA_MYCLE	P25014 cyanophora
28	35	50.0	625	1 BAR3_SCHCO	P46392 mycobacteri
29	35	50.0	715	1 ADSV_BOVIN	Q28046 bos taurus
30	35	50.0	715	1 ADSV_HUMAN	Q9y6u3 homo sapien
31	35	50.0	760	1 OCVL_XENLA	P16143 xenopus lae
32	35	50.0	1069	1 C910_HUMAN	Q9nab2 homo sapien
33	35	50.0	1736	1 ZOL_HUMAN	Q07157 homo sapien

34	35	50.0	1745	1 ZOL_MOUSE	P39447 mus musculu
35	35	50.0	1782	1 VITR_BOMMO	Q27309 bombyx mori
36	34.5	49.3	96	1 RL21_METTH	Q27378 methanobact
37	34	48.6	279	1 PHEX_LACLA	P43909 lactococcus
38	34	48.6	292	1 YOW1_CAEEL	P30647 caenorhabdi
39	34	48.6	397	1 CAPB_BACAN	P19580 bacillus an
40	34	48.6	826	1 VILL_HUMAN	P09327 homo sapien
41	34	48.6	826	1 VILL_MOUSE	Q62468 mus musculu
42	34	48.6	1004	1 RPOC_OENOE	P95405 oenococcus
43	34	48.6	1053	1 RPOC_LTSIN	P77879 listeria in
44	34	48.6	1077	1 XYNX_CLOTM	P51584 clostridium
45	34	48.6	1355	1 CA21_RANCA	Q42350 rana catesb

## ALIGNMENTS

RESULT	1	STANDARD:	PRT:	106 AA.
KAC_HUMAN				
ID	KAC_HUMAN			
AC	P01834;			
DT	21-JUL-1986 (rel. 01, Created)			
DT	21-JUL-1986 (rel. 01, Last sequence update)			
DT	20-AUG-2001 (rel. 40, Last annotation update)			
DE	IG KAPPA CHAIN C REGION.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MVELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RT	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RT	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hieber P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RT	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess W., Langer B., Ponslingl H.,			
RT	Stelimeitz-Kayne M., Suter L., Watanabe S.;			
RT	(in) Finek F., Shugar D. (eds.);			
RT	Gamma globulins: structure and function, pp.57-74, Academic Press,			
RT	New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."			

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).  
RN [7]  
RP SEQUENCE (BENCE-JONES PROTEIN AC).  
RX MEDLINE-69234734; PubMed-4893682;  
RA Titani K., Shioda T., Putnam F.W.:  
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The  
RL complete sequence and the location of the disulfide bridges".  
RL J. Biol. Chem. 244:3550-3560(1969).  
RN [8]  
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN CU).  
RX MEDLINE-70201507; PubMed-5447531;  
RA Kohler H., Shimizu A., Paul C., Putnam F.W.:  
RT "Macroglobulin structure: variable sequence of light and heavy  
RT chains".  
RL Science 169:56-59(1970).  
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,  
CC 45-ALA 6 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC  
CC MARKER, 45-ALA AND 83-LEU.  
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CC -----  
DR EMBL: J00241; AAA58989.1; -;  
DR EMBL: V00557; CAA23823.1; -;  
DR PIR: A02116; K3HU.  
DR MTM: 147200; -;  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003597; Ig\_cl.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00407; Igcl.1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region.  
KW NON\_TER 1  
FT DISULFID 26 86  
FT DISULFID 106 106  
FT VARIANT 83 83  
FT VARIANT /FTID-VAR 003897  
FT CONFLICT 14 14 D->N (IN REF. 7 AND 8).  
FT CONFLICT 37 37 E->Q (IN REF. 5 AND 6).  
FT CONFLICT 57 57  
SQ SEQUENCE 106 AA; 11609 MW; 51984DIPDD372CE8 CRC64;  
  
Query Match 100.0%; Score 70; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SSPVTKSFNRGEC 13  
Db 94 SSPVTKSFNRGEC 106  
|||||  
KACB\_RAT  
ID KACB\_RAT STANDARD; PRT; 106 AA.  
AC P01836;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN C REGION, A ALLELE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DA;  
RX MEDLINE-82082587; PubMed-6273908;  
RA Sheppard H.W., Gutman G.A.;

RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
DR PIR: A02118; K1RTA.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003597; Ig-cl.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00407; Igcl.1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT DISULFID 26 86  
FT DISULFID 106 106  
FT VARIANT 83 83  
FT VARIANT /FTID-VAR 003897  
FT CONFLICT 14 14 D->N (IN REF. 2).  
FT CONFLICT 37 37 E->Q (IN REF. 2).  
FT CONFLICT 57 57  
SQ SEQUENCE 106 AA; 11732 MW; B7E120D970DD066 CRC64;  
  
Query Match 84.3%; Score 59; DB 1; Length 106;  
Best Local Similarity 84.6%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 SSPVTKSFNRGEC 13  
Db 94 SSPVTKSFNRGEC 106  
|||||  
KACB\_RAT  
ID KACB\_RAT STANDARD; PRT; 106 AA.  
AC P01835;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN C REGION, B ALLELE.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LOU;  
RX MEDLINE-82082587; PubMed-6273908;  
RA Sheppard H.W., Gutman G.A.;  
RT "Allelic forms of rat kappa chain genes: evidence for strong  
RT selection at the level of nucleotide sequence."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).  
RN [2]  
RP SEQUENCE (BENCE-JONES PROTEIN S211).  
RX MEDLINE-75212238; PubMed-807630;  
RA Starace V., Querinjean P.;  
RT phylogenetic relationships of a rat kappa Bence Jones protein;  
RL J. Immunol. 115:59-62(1975).  
DR PIR: A02117; K1RTB.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003597; Ig-cl.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00407; Igcl.1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT DISULFID 26 86  
FT DISULFID 106 106  
FT CONFLICT 2 2 D->N (IN REF. 2).  
FT CONFLICT 30 30 N->K (IN REF. 2).  
FT CONFLICT 48 48 MISSING (IN REF. 2).  
FT CONFLICT 79 79 E->Q (IN REF. 2).  
FT CONFLICT 87 87 E->Q (IN REF. 2).  
FT CONFLICT 98 98 V->W (IN REF. 2).  
FT CONFLICT 100 100 S->N (IN REF. 2).  
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;  
  
Query Match 84.3%; Score 59; DB 1; Length 106;

Best Local Similarity 84.6%; Pred. No. 0.00019;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 SSPVTKSFNRNEC 106

RESULT 4

KAC\_MOUSE STANDARD: PRT: 106 AA.

AC P01837;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE IG KAPPA CHAIN C REGION.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxId=10090;

RN [11] SEQUENCE (MOC 21).

RP MEDLINE=73053310; PubMed=4638343;

RA Svasti J., Milstein C.;

RT "The complete amino acid sequence of a mouse kappa light chain.";

RL Biochem. J. 128:427-444(1972).

RN [12] DISULFIDE BONDS (MOC 21).

RP MEDLINE=73008889; PubMed=5073237;

RA Svasti J., Milstein C.;

RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";

RL Biochem. J. 126:837-850(1972).

RN [13] SEQUENCE FROM N.A., AND REVISIONS TO 53-59.

RP MEDLINE=79084137; PubMed=103625;

RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;

RT "Complete sequence of constant and 3' noncoding regions of an

immunoglobulin mRNA using the dideoxynucleotide method of RNA

sequencing.";

RL Cell 15:1067-1075(1978).

RN [14] SEQUENCE FROM N.A.

RP MEDLINE=82059477; PubMed=6170937;

RA Hamlyn P.H., Gait M.J., Milstein C.;

RT "Complete sequence of an immunoglobulin mRNA using specific priming

and the dideoxynucleotide method of RNA sequencing.";

RL Nucleic Acids Res. 9:4485-4494(1981).

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DR EMBL: V00807; CAA24189.1; -

DR PIR: A02119; KIMS.

DR PIR: S01320; S01320.

DR MGI: 96495; I9K-C.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003597; Ig\_c1.

DR Pfam: PF00047; Ig\_1.

DR SMART: SM00407; Igcl: 1.

DR PROSITE: PS00290; Ig\_MHC, 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON\_TER 1

FT DISULFID 26 86

FT DISULFID 106 106

FT SEQUENCE 106 AA; 11778 MW; 4B51F5EF49BA85 CRC64;

INTERCHAIN (WITH A HEAVY CHAIN).

Query Match

Best Local Similarity 78.6%; Score 55; DB 1; Length 106;

Matches 9; Conservative 69.2%; Pred. No. 0.0011;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 TSPVTKSFNRNEC 106

RESULT 5

KACB\_RABIT STANDARD: PRT: 106 AA.

ID P01839;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA-B4 CHAIN C REGION.

K-BAS.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

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CC -----

DR EMBL: V00807; CAA24189.1; -

DR PIR: A02119; KIMS.

DR PIR: S01320; S01320.

DR MGI: 96495; I9K-C.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003597; Ig\_c1.

DR Pfam: PF00047; Ig\_1.

DR SMART: SM00407; Igcl: 1.

DR PROSITE: PS00290; Ig\_MHC, 1.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON\_TER 1

FT DISULFID 26 86

FT DISULFID 106 106

FT SEQUENCE 106 AA; 11778 MW; 4B51F5EF49BA85 CRC64;

INTERCHAIN (WITH A HEAVY CHAIN).

Query Match

Best Local Similarity 78.6%; Score 55; DB 1; Length 106;

Matches 9; Conservative 69.2%; Pred. No. 0.0011;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNRGEC 13

Db 94 TSPVTKSFNRNEC 106

RESULT 5

KACB\_RABIT STANDARD: PRT: 106 AA.

ID P01839;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

IG KAPPA-B4 CHAIN C REGION.

K-BAS.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

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FO  DISULFID  106  106  INTERCHAIN (WITH A HEAVY CHAIN) .
FT  SEQUENCE  106 AA: 11279 MW: 499B928DDA853849 CRC64:

Query Match 77.1%, Score 54; DB 1; Length 106;
Best Local Similarity 61.5%; Pred. No. 0.0018;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY  1 SSPVTKSPNRGEC 13
DB  94 ASPVQSFNRGDC 106

RESULT  6
KAC4_RABIT
AC  P01840; STANDARD: PRT; 103 AA.
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  IG_KAPPA-B94 CHAIN C REGION.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=83300036; PubMed=6412231;
RA  Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
RT  "Rabbit immunoglobulin kappa genes: structure of a germline b4
RT  allele type J-C locus and evidence for several b4-related sequences in
RT  the rabbit genome.";
RL  Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=82060334; PubMed=6795636;
RA  Heldmann O., Auffray C., Cazenave P.-A., Rougeon F.;
RT  "Nucleotide sequence of constant and 3' untranslated regions of a
RT  kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
RL  Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
RN  [3]
RP  SEQUENCE.
RX  MEDLINE=75133568; PubMed=1091650;
RA  Chen K.C.S., Kindt T.J., Krause R.M.;
RT  "Primary structure of the L chain from a rabbit homogeneous antibody
RT  to streptococcal carbohydrate. II. Sequence determination of peptides
RT  from tryptic and peptic digests.";
RL  J. Biol. Chem. 250:3289-3296(1975).
CC  -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE
CC  SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM
CC  THE SERUM OF A SINGLE RABBIT.
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DR  EMBL: X00231; CAA25051.1; -.
DR  PTR: A02122; KARB.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003597; Ig_cl.
DR  Pfam: PF00047; Ig; 1.
DR  SMART: SM00407; IGC1; J.
DR  PROSITE: PS00290; IG_MHC; FALSE_NEG.
DR  Immunoglobulin domain; Immunoglobulin C region.
KW  NON_TER 1
FT  DISULFID 26 85. INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 103 103. N -> D (IN REF. 3).
FT  CONFLICT 58 58.
FO  SEQUENCE 103 AA: 11043 MW: 5FC5ACCB86068DB CRC64:

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QY      1 SSPVTKSFNRGEC 13          62.9%: Score 44; DB 1; Length 103;
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Db      91 TTSVVSFNRGDC 103         53.8%: Pred. NO. 0.15;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 7
ID      KAC9_RABIT    STANDARD:   PRT:   104 AA.
AC      P01838;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA-B9 CHAIN C REGION.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota, Metazoa, Chordata; Craniata; Vertebrate; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN      NCBI_Taxid=9986;
RP      SEQUENCE.
RX      MEDLINE=76176480; PubMed=817288;
RA      Farnsworth V., Goodfiliash R., Rodkey S., Hood L.;
RT      "Immunoglobulin allotypes of rabbit kappa chains: polymorphism of a
RL      control mechanism regulating closely linked duplicated genes?";
RL      Proc. Natl. Acad. Sci. U.S.A. 73:1293-1296(1976).
CC      -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM POOLED IMMUNOGLOBULIN
           OF HOMOLOGOUS B9 RABBITS.
DR      PIR, A02120; K9RB.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003597; IG_cl.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00407; Igcl; 1.
KW      PROSITE; PS00290; IG-MHC; FALSE_NEG.
KW      Immunoglobulin domain; Immunoglobulin C region.
FT      NON_TER      1
FT      DISULFD      27      86
FT      DISULFD      104     104      INTERCHAIN (WITH A HEAVY CHAIN).
SQ      SEQUENCE     104 AA; 11347 MW; 427B16B8B0EC8D98 CRC64;

Query Match          60.0%; Score 42; DB 1; Length 104;
Best Local Similarity 60.0%; Pred. NO. 0.36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      4 YTKSFRNGEC 13          :|:|||||:|
Db      95 IVTSFNRGDC 104

RESULT 8
ID      YCWL_YEAST    STANDARD:   PRT:   121 AA.
AC      P25642;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      HYPOTHEETICAL 13.6 KDA PROTEIN IN CPK4-SKR22 INTERGENIC REGION.
GN      YCR071C OR YCR71C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Sacchariomyces.
RN      NCBI_Taxid=4932;
RP      SEQUENCE FROM N.A.
RA      Ballesta J.P.G., Franco L., Hoenicka J., Jimenez A., Remacha M.,
RA      Sanz E.;
RL      Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
CC      -I- SIMILARITY: SOME, TO S.POMBE SPAC3H8.03.
```

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CC -----
DR EMBL: X59720; CAA42269.1; -
DR PIR: S19486; S19486.
DR SGD: S0000667; IMG2.
DR Hypothetical protein.
SO SEQUENCE 121 AA; 13682 MW; F8E3304D6F38475A CRC64;

Query Match      60.0%; Score 42; DB 1; Length 121;
Best Local Similarity 61.5%; Pred. No. 0.42;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SSPVTKSFNRGEC 13
   11 11 11 11 11
Db 3 SSCVTRCFGRGKC 15

RESULT 9
GELS_PIG
ID GELS_PIG STANDARD; PRT; 772 AA.
AC P20305;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLIMERIZING FACTOR) (ADF)
GN (BREVIN) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89094858; PubMed=2850369;
RA Way M., Weeds A.G.;
RT "Nucleotide sequence of pig plasma gelsolin. Comparison of protein
RT sequence with human gelsolin and other actin-severing proteins shows
RT strong homologies and evidence for large internal repeats."
RL J. Mol. Biol. 203:1127-1133(1988).
RN [2]
RP SEQUENCE OF 34-72.
RX MEDLINE=87054019; PubMed=3023087;
RA Weeds A.G., Gooch J., Pope B., Harris H.E.;
RT "Preparation and characterization of pig plasma and platelet
RT gelsolins."
RL Eur. J. Biochem. 161:69-76(1986).
CC -1- FUNCTION: CALCIUM-REGULATED, ACTIN-MODULATING PROTEIN THAT BINDS
CC TO THE PLUS (OR BARBED) ENDS OF ACTIN MONOMERS OR FILAMENTS,
CC PREVENTING MONOMER EXCHANGE (END-BLOCKING OR CAPPING). IT CAN
CC PROMOTE THE ASSEMBLY OF MONOMERS INTO FILAMENTS (NUCLEATION) AS
CC WELL AS SEVER FILAMENTS ALREADY FORMED.
CC -1- SUBUNIT: BINDS TO ACTIN AND TO FIBRONECTIN.
CC -1- SUBCELLULAR LOCATION: SECRETED (PLASMA FORM) AND CYTOPLASMIC.
CC -1- ALTERNATIVE PRODUCTS: PLASMA GELSOLIN AND CYTOPLASMIC GELSOLIN
CC ARE DERIVED FROM A SINGLE GENE BY ALTERNATE INITIATION SITES AND
CC DIFFERENTIAL SPLICING.
CC -1- SIMILARITY: BELONGS TO THE VILIN/GELSOLIN FAMILY.
CC -1- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
CC -----
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CC -----
DR EMBL: M36927; AAA31042.1; -
DR EMBL: X13871; CAA32077.1; -
DR PIR: S02665; S02665.
DR PIR: A25308; A25308.
DR PIR: B25308; B25308.
DR HSP: P06396; 1SOL.
DR InterPro: IPR001974; Gelsolin.
DR Pfam: PF00626; Gelsolin; 6.
DR SMART: SM00262; GEL; 6.
KW Cytoskeleton; Actin-binding; Repeat; Calcium; Alternative splicing;
KW Signal; Capping protein.
FT NON_TER 1 1
FT SIGNAL <1 17
FT PROPEP 18 33
FT CHAIN 34 772
FT CHAIN 43 772
FT DOMAIN 41 166
FT DOMAIN 424 772
FT REPEAT 66 116
FT REPEAT 188 228
FT REPEAT 304 346
FT REPEAT 443 494
FT REPEAT 566 606
FT REPEAT 669 711
FT SITE 113 116
FT SITE 152 159
FT SITE 178 186
FT SITE 205 218
FT DISULFID 38 38
FT CONFLICT 38 38
FT CONFLICT 772 AA; 84775 MW; B5611DB9D541BF9 CRC64;
SO SEQUENCE

Query Match      57.9%; Score 40.5; DB 1; Length 772;
Best Local Similarity 66.7%; Pred. No. 5.9;
Matches 8; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 3 PVT-KSFNRGEC 13
   11 11 11 11 11
Db 194 PVSWSFNRGDC 205

RESULT 10
KAC6_RABIT
ID KAC6_RABIT STANDARD; PRT; 104 AA.
AC P03984;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN B5 VARIANT C REGION.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A. (CLONE PKB5-F2).
RX MEDLINE=84041515; PubMed=6314281;
RA Bernstein K.E., Skurja R.M., Jr., Mage R.G.;
RT "The sequences of rabbit kappa light chains of b4 and b5 allotypes
RT differ more in their constant regions than in their 3' untranslated
RT regions."
RL Nucleic Acids Res. 11:7205-7214(1983).
CC -1- MISCELLANEOUS: THE CDNA FROM WHICH THIS SEQUENCE WAS DERIVED
CC CONTAINS A TERMINATOR CODON WITHIN THE V-REGION CODING REGION. THE
CC ORIGIN OF THIS CODON AND OF THE DIFFERENCES BETWEEN THIS AND OTHER
CC SEQUENCED B5 C REGIONS ARE UNCLEAR. THE CDNA CLONE WAS MADE USING
CC mRNA FROM TRYPAANOSOME-INJECTED B5-HOMOZYGOUS RABBITS.
CC -----
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DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE UDP-N-ACETYLTRANSFERASE-2,6-DIAMINOPYRIMIDINE-2,6-DIHYDROLYASE  
 DE ALANINE LIGASE (EC 6.3.2.15) (UDP-MURNAAC-PENTAPEPTIDE SYNTHETASE)  
 DE (D-ALANINE-D-ALANINE-ADDING ENZYME).  
 GN MURF OR BU220.  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 symbiotic bacterium).  
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
 OX NCBI\_TaxID=118099;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TOXO 1998;  
 RX MEDLINE=20445173; PubMed=10993077;  
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT Genome sequence of the endocellular bacterial symbiont of aphids  
 RT Buchnera sp. Aps.;  
 RL Nature 407:81-86(2000).  
 CC -1- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYZES THE FINAL  
 CC STEP IN THE SYNTHESIS OF UDP-N-ACETYLURAMONYL-PENTAPEPTIDE, THE  
 CC PRECURSOR OF MUREIN (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMONYL-L-ALANYL-D-GLUTAMYL  
 CC -MESO-2,6-DIAMINOPYRIMIDINATE + D-ALANYL-D-ALANYL - ADP +  
 CC ORTHOPHOSPHATE + UDP-N-ACETYLURAMONYL-L-ALANYL-D-GAMMA-GLUTAMYL-6-  
 CC CARBOXY-L-LYSYL-D-ALANYL-D-ALANINE.  
 CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF011118; BMB12936.1; -  
 DR InterPro: IPR000713; Mur\_Ligase.  
 DR Pfam: PF01225; Mur\_Ligase.1.  
 KW Peptidoglycan synthesis; Cell division; Cell wall; Ligase;  
 KM ATP-binding; Complete proteome.  
 FT NP\_BIND 107 113  
 FT SEQUENCE 455 AA; 50451 MW; E292D8E9290E67B7 CRC64;  
 SQ  
 Query Match 52.9%; Score 37; DB 1; Length 455;  
 Best Local Similarity 58.3%; Pred. No. 16;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 SSPVTKSFNRC 12  
 Db 395 SSEITKIFNNGK 406  
 RESULT 13  
 YAS4\_METUA  
 ID YAS4\_METUA STANDARD; PRT; 895 AA.  
 AC 058454;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HYPOTHETICAL PROTEIN MJ1054 (EC 1.1.1.-).  
 GN MJ1054.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
 OC Methanococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE=96337999; PubMed=8688087;  
 RA Bull C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kertland A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merriam J.M., Glodek A.,  
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,  
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurt M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT Complete genome sequence of the methanogenic archaeon, Methanococcus  
 RT jannaschii.;  
 RL Science 273:1058-1073(1996).  
 CC -1- SIMILARITY: BELONGS TO THE UDP-GLUCOSE/GDP-MANNANOSE DEHYDROGENASES  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U67548; AAB99056.1; -  
 DR TIGR: MJ1054; -  
 DR InterPro: IPR003586; Hinc.  
 DR InterPro: IPR003587; Hinc.  
 DR InterPro: IPR00205; NAD\_binding.  
 DR InterPro: IPR001732; UDPG\_MGDP\_dh.  
 DR Pfam: PF00984; UDPG\_MGDP\_dh.1.  
 DR SMART: SM00305; Hinc.1.  
 DR SMART: SM00306; Hinc.1.  
 DR Hypothetical protein; Oxidoreductase; NAD: Complete proteome.  
 KW NP\_BIND 2 19  
 FT ACT\_SITE 261 261  
 FT NAD SIMILARITY.  
 FT SEQUENCE 895 AA; 102614 MW; B511AA68CCA41445 CRC64;  
 SQ  
 Query Match 52.9%; Score 37; DB 1; Length 895;  
 Best Local Similarity 75.0%; Pred. No. 33;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Oy 6 KSFNRCGEC 13  
 Db 37 KALNRGEC 44  
 RESULT 14  
 CHRL\_BOMMO  
 ID CHRL\_BOMMO STANDARD; PRT; 177 AA.  
 AC P13532;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-JAN-1990 (Rel. 13, Last annotation update)  
 DE CHORION PROTEIN ERB.1 PRECURSOR.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Bombycoidea; Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88112521; PubMed=3338621;  
 RA Hübner B.L., Burke W.D., Lecanidou R., Rodakis G.C., Eickbush T.H.;  
 RT "Organization and expression of three genes from the silkworm early  
 RT chorion locus".  
 RL Dev. Biol. 125:423-431(1988).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE  
 CC SILK MOTH.  
 CC -----  
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DR EMBL: M19077; AAA27832.1; -  
DR PIR: C45937; C45937.  
DR InterPro: IPR002635; Chorton.  
DR Pfam: PF01723; Chorton; 1.  
KW Eggshell; Chorton; Repeat; Multigene family; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 177 CHORION PROTEIN ERB.1.  
SQ SEQUENCE 177 AA; 17034 MW; 3227F195C55A8B6F CRC64;

Query Match 51.4%; Score 36; DB 1; Length 177;  
Best Local Similarity 60.0%; Pred. No. 9.1;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 2 SPVTKSFNRG 11  
Db 159 APLGRSFNRG 168

RESULT 15  
MTD2\_HERAU STANDARD; PRT; 354 AA.  
AC P25265;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE MODIFICATION METHYLASE HGDI1 (EC 2.1.1.73) (CYTOSINE-SPECIFIC  
DE METHYLTRANSFERASE HGDI1) (M. HGDI1).  
GN HGDI1.  
OS Herpesosiphon aurantiacus (Herpesosiphon giganteus).  
OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;  
OC Herpesosiphon.  
OX NCBI\_Taxid=65;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPA2;  
RX MEDLINE=92039068; Pubmed=1937045;  
RA Duesterhoeft A., Kroeger M.;  
RT "Cloning, sequence and characterization of m5C-methyltransferase-  
RT encoding gene, hgid1m (GTCGAC), from Herpesosiphon giganteus strain  
RT Hpa2.";  
RL Gene 106:87-92(1991).  
RN [2]  
RP DISCUSSION OF SEQUENCE.  
RX MEDLINE=9531598; Pubmed=7607523;  
RA Kroeger M., Blum E., Deppe E., Duesterhoeft A., Erdmann D., Kilz S.,  
RA Meyer-Rogge S., Moestl D.;  
RT "Organization and gene expression within restriction-modification  
RT systems of Herpesosiphon giganteus.";  
RL Gene 157:43-47(1995).  
CC -!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE  
CC GTCGAC, CAUSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS AND  
CC PROTECTS THE DNA FROM CLEAVAGE BY THE HGDI1 ENDONUCLEASE.  
CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE =  
CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.  
CC -!- SIMILARITY: STRONG. TO OTHER C5-DNA METHYLASES.  
CC -----  
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DR PIR: S21952; S21952.  
DR REBASE: 3418; M.HgDI1.  
DR InterPro: IPR001525; C5\_DNA\_meth.  
DR Pfam: PF00145; DNA\_methylase; 1.  
DR PROSITE: PS00094; C5\_MTASE.1; 1.  
DR PROSITE: PS00095; C5\_MTASE.2; 1.  
KW Transferase; Methyltransferase; Restriction system.  
FT ACT\_SITE 75 75  
FT ACT\_SITE 75 75  
SQ SEQUENCE 354 AA; 39853 MW; BDA017785D5AD75 CRC64;

Query Match 51.4%; Score 36; DB 1; Length 354;  
Best Local Similarity 60.0%; Pred. No. 19;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PVTKSFNRG 12  
Db 119 PEVTRFNRG 128

Search completed: January 4, 2002, 18:14:38  
Job time: 297 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 4, 2002, 18:13:57 : Search time 37.65 Seconds  
(without alignments)

50,506 Million cell updates/sec

Title: US-09-875-221A-113

Sequence: 1 SSPVTKSFNRGEC 13

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Database : SPTREMBL 17:17  
Listing first 45 summaries

1: sp\_archaea:\*\*\*  
2: sp\_bacteria:\*\*\*  
3: sp\_fungi:\*\*\*  
4: sp\_human:\*\*\*  
5: sp\_invertebrate:\*\*\*  
6: sp\_mammal:\*\*\*  
7: sp\_mmc:\*\*\*  
8: sp\_organelle:\*\*\*  
9: sp\_phage:\*\*\*  
10: sp\_plant:\*\*\*  
11: sp\_rodent:\*\*\*  
12: sp\_virus:\*\*\*  
13: sp\_vertebrate:\*\*\*  
14: sp\_unclassified:\*\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	78.6	238	11 099M37	099M37 mus musculus
2	50	71.4	214	11 099A15	099A15 mus musculus
3	40	57.1	548	5 062019	062019 caenorhabditis
4	40	57.1	1111	5 09W008	09W008 drosophila
5	39	55.7	821	10 091L17	091L17 zea mays (m
6	38	54.3	74	4 09H550	09H550 homo sapien
7	38	54.3	108	4 09H551	09H551 homo sapien
8	38	54.3	258	2 09RST9	09RST9 delinococcus
9	38	54.3	279	3 09US20	09US20 schizosacch
10	38	54.3	523	4 099993	099993 homo sapien
11	38	54.3	553	10 09T0J7	09T0J7 arabidopsis
12	38	54.3	569	4 09BXR6	09BXR6 homo sapien
13	38	54.3	3012	4 09Y3N6	09Y3N6 homo sapien
14	37	52.9	67	9 080307	080307 bacterioph
15	37	52.9	219	4 09UDK7	09UDK7 homo sapien
16	37	52.9	295	12 09YLP1	09YLP1 human coxa
17	37	52.9	296	12 09YLM5	09YLM5 human coxa
18	37	52.9	352	10 09SD61	09SD61 arabidopsis
19	37	52.9	409	2 067129	067129 aquifex aeo

20	37	52.9	494	5 044649	044649 caenorhabdi
21	37	52.9	717	10 09LUR4	09LUR4 arabidopsis
22	37	52.9	1028	10 09C6A5	09C6A5 arabidopsis
23	37	52.9	1309	10 09SR66	09SR66 arabidopsis
24	37	52.9	1340	10 09LTT9	09LTT9 arabidopsis
25	37	52.9	1344	10 09LTT8	09LTT8 arabidopsis
26	36	51.4	160	2 09X357	09X357 bacillus an
27	36	51.4	187	10 092951	092951 arabidopsis
28	36	51.4	230	2 053894	053894 mycobacteri
29	36	51.4	302	10 09C5F2	09C5F2 arabidopsis
30	36	51.4	347	12 09DMC8	09DMC8 rat cytoleg
31	36	51.4	356	10 09M0G2	09M0G2 arabidopsis
32	36	51.4	469	2 0912K9	0912K9 pseudomonas
33	36	51.4	473	2 005198	005198 rhizobium m
34	36	51.4	550	5 09XX90	09XX90 caenorhabdi
35	36	51.4	591	2 09Y122	09Y122 corneobacte
36	36	51.4	600	2 096890	096890 mycobacteri
37	36	51.4	615	11 008990	008990 mus musculu
38	36	51.4	627	2 097041	097041 leptospira
39	36	51.4	665	11 09R1X3	09R1X3 mus musculu
40	36	51.4	665	11 09EQH1	09EQH1 ratius norv
41	36	51.4	666	11 09Z1S8	09Z1S8 mus musculu
42	36	51.4	673	5 09VD18	09VD18 drosophila
43	36	51.4	796	5 010953	010953 caenorhabdi
44	36	51.4	895	6 09BDV9	09BDV9 lepus capen
45	36	51.4	930	4 09NY77	09NY77 homo sapien

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	238 AA.
099M37	1	099M37		
AC	099M37	099M37		
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	UNKNOWN (PROTEIN FOR MGC:5947).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=MAMMARY TUMOR;			
RA	Strausberg R.;			
RL	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: BC002035; AA02035.1; -			
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;			
Query Match	78.6%;	Score 55;	DB 11;	Length 238;
Best Local Similarity	69.2%;	Pred. No. 0.011;		
Matches	9;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	1 SSPVTKSFNRGEC 13			
DB	226 TSPIVKSFNNGEC 238			
RESULT	2			
ID	099A15	PRELIMINARY:	PRT:	214 AA.
AC	099A15			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.:  
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFv)".  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1. SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF152371; AAD40242.1; -  
 DR HSSP: P01789; IMCP  
 DR InterPro: IPR003360; IG\_like  
 DR InterPro: IPR003006; IG\_MHC  
 DR InterPro: IPR003596; IG\_V  
 DR Pfam: PF00047; Ig; 2  
 DR SMART: SM00406; Igv; 1  
 DR SMART: SM00410; IG\_like; 1  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1  
 DR NON\_TER 1  
 FT 1 214  
 FT NON\_TER 1  
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE95E2A CRC64;

Query Match	71.4%	Score 50;	DB 11;	Length 214;
Best Local Similarity	61.5%	Pred. No. 0.091;		
Matches	8;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	1	SSPVTKSFNRGEC	13	
	:	111	11	
Db	202	TSPIVCKCFNRNEC	214	

RESULT	3			
062019				
ID	062019	PRELIMINARY;	PRT;	548 AA.
AC	062019;			
DT	01-AUG-1998 (TReMBLrel. 07, Created)			
DT	01-AUG-1998 (TReMBLrel. 07, Last sequence update)			
DT	01-JAN-1999 (TReMBLrel. 09, Last annotation update)			
DE	B0462.1 PROTEIN.			
GN	B0462.1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_Taxid=6239;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mortimore B.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94150716; PubMed=7906398;			
RA	Wilson R., Alnscough R., Andersson K., Baynes C., Berks M.,			
RA	Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,			
RA	Craxton M., Dear S., Du Z., Durbin R., Favetto A., Fulton L.,			
RA	Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,			
RA	Jones M., Keshav J., Kirsten J., Laister N., Laister P.,			
RA	Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,			
RA	Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen R.,			
RA	Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,			
RA	Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,			
RA	Watson A., Weinstein L., Wilkenson-Sproat J., Wohlman P.;			
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.			
RT	elegans";			
RL	Nature 368:37-38(1994).			
DR	EMBL: Z81456; CAB03810.1;			
DR	SEQUENCE 548 AA; 63199 MW; 66368C07E7ACCA13 CRC64;			

Query Match	57.1%;	Score 40;	DB 5;	Length 548;
Best Local Similarity	61.5%;	Pred. No. 20;		
Matches	8;	Conservative	1;	Mismatches 4;
				Indels 0;
				Gaps 0;

OY	1	SSPVKSFNREGC	13
	1	1	11
DB	403	SGNYLKSIDRREC	415
RESULT	4		
Q9W008			
Q9W008		PRELIMINARY;	PRT; 1111 AA.
AC	Q9W008		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	CG1141	PROTEIN.	
GN	CG1141.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Empidoidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

RX MEDLINE-20196006; PubMed-107311137;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Miller B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abvri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Baller R.M., Basu A.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,  
 RA Botkova D., Botkov M.R., Butler H., Brinkstein P., Brothier P.,  
 RA Burks K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacble J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheele F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Wodade T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zavadil J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong G.M., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*."  
 RT Science 287:2185-2195(2000).  
 RL EMBL: AEO03475: AAF47652.1; -;  
 DR HSSP: P02640; IVII.  
 DR FLYbase: FBgn00035347; CG1141.  
 DR InterPro: IPR001974; Gelsolin.  
 DR InterPro: IPR003128; VHP.  
 DR Pfam: PF00626; Gelsolin; 1.  
 DR Pfam: PF02209; VHP; 1.  
 DR PRINTS: PR00597; GELSOLIN.  
 DR SMART: SM00262; GEL; 4.  
 DR SMART: SM00153; VHP; 1.  
 QO SEQUENCE 1111 AA; 126001 MW; 186BD07B969E23B63 CRC64;

Query Match 57.1%; Score 40; DB 5; Length 1111;  
Best Local Similarity 63.6%; Pred. NO. 40;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 PVTKSFNRGEC 13  
DB 337 PVTSLNRGDC 347

RESULT 5

09L17 PRELIMINARY; PRT; 821 AA.  
AC 09L17;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
GN CELULOSE SYNTHASE-3 (FRAGMENT).  
OS CESA-3.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dhuga K.S., Helentjaris T.G.;  
RT "Cellulose synthase-3 (Cesa-3) cDNA from maize."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF200527; AAF89963.1;  
FT NON\_TER 1  
SQ SEQUENCE 821 AA; 92900 MW; DB2AFE50807A0B0 CRC64;

Query Match 55.7%; Score 39; DB 10; Length 821;  
Best Local Similarity 50.0%; Pred. NO. 46;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 SPVTKSFNRGEC 13  
DB 806 SPYKALSRGOC 817

RESULT 6

09H550 PRELIMINARY; PRT; 74 AA.  
AC 09H550;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE BA207N4.1.3 (NOVEL PROTEIN (MUSC-H\_263A.1 (TR:Q99993)) (ISOFORM 3))  
GN (FRAGMENT).  
GN BA207N4.2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Phillimore B.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL137143; CAC10455.1;  
FT NON\_TER 74  
SQ SEQUENCE 74 AA; 8503 MW; 999B9F5E0A0A0AF3 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 74;  
Best Local Similarity 70.0%; Pred. NO. 6.6;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVTKSFNRGEC 12  
DB 59 PLTKSLRGEC 68

RESULT 7  
09H551 PRELIMINARY; PRT; 108 AA.  
ID 09H551;  
AC 09H551;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE BA207N4.1.1 (NOVEL PROTEIN (TRANSLATION OF CDNAS EM:U50534 AND  
EM:AL049784) (ISOFORM 1)) (FRAGMENT).  
GN BA207N4.2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Phillimore B.;  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL137143; CAC10454.1;  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 12060 MW; 8E3FCBF7FC599D41 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 108;  
Best Local Similarity 70.0%; Pred. NO. 9.6;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVTKSFNRGEC 12  
DB 93 PLTKSLRGEC 102

RESULT 8  
09RST9 PRELIMINARY; PRT; 258 AA.  
ID 09RST9;  
AC 09RST9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE AMINOGLYCOSIDE N3'-ACETYLTRANSFERASE, TYPE IV.  
GN DR2034.  
OS Deinococcus radiodurans.  
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
OX NCBI\_TaxID=1299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20036896; PubMed=10567266;  
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
RA Fraser C.M.;  
RT "Genome sequence of the radioresistant bacterium Deinococcus  
radiodurans R1."  
RL Science 286:1571-1577(1999).  
DR EMBL; AE002040; AAF11584.1;  
DR TIGR; DR2034;  
DR InterPro; IPR003679; Antibiotic\_NAT.  
DR Pfam; PF02522; Antibiotic\_NAT.1.  
SQ SEQUENCE 258 AA; 28432 MW; D2C3A544ADC3230 CRC64;

Query Match 54.3%; Score 38; DB 2; Length 258;  
Best Local Similarity 80.0%; Pred. NO. 23;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSPVTKSFNR 10

Db 66 SSPVASFNR 75

## RESULT 9

ID Q9US20 PRELIMINARY: PRT: 279 AA.

AC Q9US20: 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PUTATIVE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE.  
 GN SPAC181.02.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972H-;  
 RA Mcougal R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AL133361, CAB82428.1; -  
 DR InterPro: IPR002123; Acyltransferase.  
 DR Pfam: PF01553; Acyltransferase.1.  
 DR Transferase; Acyltransferase.  
 KW SEQUENCE 279 AA; 31393 MM; E560D3366C9A0B63 CRC64;

## Query Match

Best Local Similarity 54.3%; Score 38; DB 3; Length 279;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PYTKSFNRGE 12  
 Db 224 PPTKVFNRKE 233

## RESULT 10

ID Q99993 PRELIMINARY: PRT: 523 AA.

AC Q99993: 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE PAC CLONE 263A.  
 GN WUGSC.H.263A.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Favella T., Ritkin L., Tatch A., Le T.T.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AC000062; AAB46343.1; -  
 SQ SEQUENCE 523 AA; 60090 MM; 52B2A6ED285F0D43 CRC64;

## Query Match

Best Local Similarity 54.3%; Score 38; DB 4; Length 523;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PYTKSFNRGE 12  
 Db 59 PLTKSLGRGE 68

## RESULT 11

ID Q9T0J7 PRELIMINARY: PRT: 553 AA.

AC Q9T0J7: 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HYPOTHETICAL 61.2 KDA PROTEIN.  
 GN T9A14.180 OR AT4G38900.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eudicots II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,  
 RA Mayer K.F.X., Scheller C.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL035656; CAB38624.1; -  
 DR EMBL: AL161594; CAB80553.1; -  
 DR InterPro: IPR001871; bZIP.  
 DR Pfam: PF00170; bZIP.1.  
 DR SMART: SM00338; BRIZ.1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 553 AA; 61156 MM; 09F72DDCC63611F2 CRC64;

## Query Match

Best Local Similarity 54.5%; Score 38; DB 10; Length 553;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 PYTKSFNRGEC 13  
 Db 190 PLERSFSGEC 200

## RESULT 12

ID Q9BXR6 PRELIMINARY: PRT: 569 AA.

AC Q9BXR6: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE COMPLEMENT FACTOR H-RELATED PROTEIN 5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11058592;  
 RA Mcrae J.L., Cowan P.J., Power D.A., Mitchellhill K.I., Kemp B.E.,  
 RA Morgan B.P., Murphy B.F.;  
 RT "Human Factor H-related Protein 5 (FHR-5). A New Complement-Associated Protein."  
 RL J. Biol. Chem. 276:6747-6754(2001).  
 DR EMBL: AF295327; AAK15619.1; -  
 SQ SEQUENCE 569 AA; 64419 MM; 7FAAE31707B0C112 CRC64;

Query Match 54.3%; Score 38; DB 4; Length 569;  
Best Local Similarity 53.8%; Pred. No. 50;  
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 SSPYTKSFNRGEC 13  
|:| | |:  
Db 135 STPEICSFTRGEC 147

## RESULT 13

OY3N6 PRELIMINARY; PRT; 3012 AA.  
ID OY3N6;  
AC OY3N6;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE HYPOTHETICAL 338.2 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rhodes S.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL049784; CAB42442.1; -;  
DR InterPro: IPR001745; GHMP\_kinase.  
DR PROSITE: PS00627; GHMP\_KINASES\_ATP; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 3012 AA; 338175 MW; 4034E2C82F7A578F CRC64;

Query Match 54.3%; Score 38; DB 4; Length 3012;  
Best Local Similarity 70.08%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVTKSFNRGE 12  
|:| | |:  
Db 93 PLTKSLQGE 102

## RESULT 14

ID O80307 PRELIMINARY; PRT; 67 AA.  
AC O80307;  
DT 01-NOV-1998 (TREMblrel. 08, Created)  
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
DE ORF23.  
OS Bacteriophage 186.  
OC viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;  
OC P2-like viruses.  
OX NCBI\_TaxID=29252;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98371265; Pubmed=9705261;  
RA Portelli R., Dodd I.B., Xue O., Egan J.B.;  
RT "The late-expressed region of the temperate coliphage 186 genome.";  
RL Virology 246:117-130(1998).  
DR EMBL: U32222; AAC34153.1; -;  
SQ SEQUENCE 67 AA; 7264 MW; 4995EFF98922D001 CRC64;

Query Match 52.9%; Score 37; DB 9; Length 67;  
Best Local Similarity 66.78%; Pred. No. 9.3;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SSPYTKSFNRGE 12  
|:| | |:  
Db 56 SSPYTKTINLME 67

## RESULT 15

O9UDK7 PRELIMINARY; PRT; 219 AA.  
ID O9UDK7;  
AC O9UDK7;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
DE PREGNANCY-ASSOCIATED PLASMA PROTEIN-A, PAPF-A (FRAGMENTS).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93286045; Pubmed=7685339;  
RA Oxvig C., Sand O., Kristensen T., Gleich G.J., Sottirup-Jensen L.;  
RT "Circulating human pregnancy-associated plasma protein-A is disulfide-  
bridged to the proform of eosinophil major basic protein.";  
RL J. Biol. Chem. 268:12243-12246(1993).  
FT NON\_TER 1 1  
FT NON\_CONS 10 11  
FT NON\_CONS 35 36  
FT NON\_CONS 63 64  
FT NON\_CONS 76 77  
FT NON\_CONS 109 110  
FT NON\_CONS 146 147  
FT NON\_CONS 161 162  
FT NON\_CONS 167 168  
FT NON\_CONS 211 212  
FT NON\_TER 219 219  
SQ SEQUENCE 219 AA; 23562 MW; 6F0DE1EDA6E5BF94 CRC64;

Query Match 52.9%; Score 37; DB 4; Length 219;  
Best Local Similarity 57.18%; Pred. No. 30;  
Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

OY 2 SPYTKSFN--RGEC 13  
|:| | |:  
Db 30 SPLTKFNFDSGEC 43

Search completed: January 4, 2002, 18:13:58  
Job time: 327 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:43:51 ; Search time 1667.48 Seconds  
(without alignments)  
801.372 Million cell updates/sec

Title: US-09-875-221A-115

Sequence: 1 gagctcaccagtaacacaaa.....gaaactgctatagcaatg 81

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_ov: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_om: \*  
20: em\_or: \*  
21: em\_ov: \*  
22: em\_pat: \*  
23: em\_ph: \*  
24: em\_pl: \*  
25: em\_ro: \*  
26: em\_sts: \*  
27: em\_sy: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htgo\_hum: \*  
31: em\_htgo\_inv: \*  
32: em\_htgo\_rod: \*  
33: em\_htg\_hum: \*  
34: em\_htg\_inv: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_other: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60.4	74.6	67	6	A97643	A97643 Sequence 10
2	35.2	43.5	1630	6	AX023367	AX023367 Sequence
3	34.2	42.2	202748	10	MMU0307670	AX0307670 Mus muscu
4	33.6	41.5	64	6	AX023342	AX023342 Sequence
5	33.4	41.2	96183	9	AL161896	AL161896 Human DNA
6	33.4	41.2	152053	2	AC022669	AC022669 Homo sapi
7	33	40.7	83599	9	AB005249	AB005249 Homo sapi
8	32.4	40.0	107526	9	HS111M5	AB005249 Human DNA s
9	32.4	40.0	216383	2	AC091273	AC091273 Mus muscu
10	32.2	39.8	57846	8	AP003053	AP003053 Oryza sat
11	32.2	39.8	108930	2	AL513122	AL513122 Human DNA
12	32.2	39.8	109422	2	AP003340	AP003340 Oryza sat
13	32.2	39.8	150380	2	AP003792	AP003792 Oryza sat
14	32.2	39.8	207392	2	AC006558	AC006558 Homo sapi
15	32	39.5	5925	6	AX009712	AX009712 Sequence
16	32	39.5	95921	9	AC004141	AC004141 Homo sapi
17	32	39.5	158758	2	AC051635	AC051635 Homo sapi
18	32	39.5	187557	2	AC069032	AC069032 Homo sapi
19	32	39.5	209462	2	AC011814	AC011814 Homo sapi
20	32	39.3	321	9	HS294735	AJ294735 Homo sapi
21	31.8	39.3	705	6	AR031183	AR031183 Sequence
22	31.8	39.3	705	6	AR042588	AR042588 Sequence
23	31.8	39.3	705	6	AR052881	AR052881 Sequence
24	31.8	39.3	705	6	AR076259	AR076259 Sequence
25	31.8	39.3	705	6	AR031185	AR031185 Sequence
26	31.8	39.3	708	6	AR042590	AR042590 Sequence
27	31.8	39.3	708	6	AR059283	AR059283 Sequence
28	31.8	39.3	708	6	AR076261	AR076261 Sequence
29	31.8	39.3	720	6	AR108864	AR108864 Sequence
30	31.8	39.3	6709	6	AX080952	AX080952 Sequence
31	31.8	39.3	7521	6	AX080951	AX080951 Sequence
32	31.8	39.3	8540	6	AR000006	AR000006 Sequence
33	31.8	39.3	8540	6	AR060919	AR060919 Sequence
34	31.8	39.3	8540	6	AX032413	AX032413 Sequence
35	31.8	39.3	8541	6	AR015960	AR015960 Sequence
36	31.8	39.3	9209	6	AR000007	AR000007 Sequence
37	31.8	39.3	9209	6	AR015961	AR015961 Sequence
38	31.8	39.3	9209	6	AR060920	AR060920 Sequence
39	31.8	39.3	9209	6	AX032414	AX032414 Sequence
40	31.8	39.3	18986	6	AR051652	AR051652 Sequence
41	31.8	39.3	18986	6	AR092290	AR092290 Sequence
42	31.8	39.3	18986	6	HSAC000363	AC000363 Human COS
43	31.8	39.3	40061	9	HSAC000354	AC000354 Human COS
44	31.8	39.3	190498	2	AC079871	AC079871 Mus muscu
45	31.8	39.3	190498	2	AC079871	AC079871 Mus muscu

## ALIGNMENTS

RESULT 1  
LOCUS A97643 67 bp DNA  
DEFINITION Sequence 10 from Patent WO915549.  
ACCESSION A97643  
VERSION A97643.1 GI:6780935  
KEYWORDS  
SOURCE unclassified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 67)  
AUTHORS Humphreys,D.P.  
TITLE Peptides  
JOURNAL Patent: WO 915549-A 10 01-APR-1999;  
CELLTECH THERAPEUTICS LTD (GB); HUMPHREYS DAVID PAUL (GB)  
FEATURES  
Source I. 67  
Location/Qualifiers  
BASE COUNT 29 a 9 c 18 g 11 t

ORIGIN

Query Match 74.6%; Score 60.4; DB 6; Length 67;  
Best Local Similarity 98.4%; Pred. No. 48e-06;  
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 gagctcacagtaacaaaagcttaataagagagatgttcagagagaataaataa 60  
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Db 6 GAGCTCACAGTAACAAAAGCTTAATAAGAGAGAGCTTGAGAGGAAAAAATGA 65  
OY 61 ag 62  
||  
Db 66 AG 67

RESULT 2

AX023367 1630 bp DNA PAT 15-SEP-2000  
DEFINITION Sequence 38 from Patent W0006605.  
ACCESSION AX023367  
VERSION AX023367.1 GI:10183779  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1630)  
AUTHORS Kufner, P., Zettl, F., Dreier, T., Baueuerle, P.A. and Borschert, K.  
TITLE Heteromindodies  
JOURNML Patent: WO 0006605-A 38 10-FEB-2000;  
KUFNER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;  
BAUEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER  
BIOMEDIZINIS (DE)

FEATURES  
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/protein\_id="CAC08836.1"  
/db\_xref="GI:10183780"

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LSCAASGETFESSGMHVRQAPGKLEAVAVISYDGSNKYYADSKRFTISRDNST  
TLTOMNSLRREDFAVYYCAKDMGMSGMPYYVGMVDMGQGTTVVSSGTPIGDNT  
HRTVAAPSVPIPPSPDOLKSCSAVYCLINNYPREAKYQKVMNALOSGQSEV  
TEODSKSTSYSLSTLTLSKADYERKHVYACEVTHOGLSEVTKSPNNGSGGGSA  
PTSSSTRKTQQLSHLLDLDMILNGINNKPKLTLNLTFRFYMPPKATKLQCL  
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BASE COUNT 445 a 410 c 408 g 367 t  
ORIGIN

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Best Local Similarity 83.3%; Pred. No. 14;  
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 gagctcacagtaacaaaagcttaataagagagatgttcagagag 48  
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Db 1154 GAGCTCACCGCGTCACAAAGAGCTTCACAGGGAGAGTTCAGAGG 1201

RESULT 3  
MMU307670/c  
LOCUS MMU307670 202748 bp DNA ROD 05-MAY-2001  
DEFINITION Mus musculus St5 gene, L27a gene and Kiaa0298 gene.  
ACCESSION AJ307670  
VERSION AJ307670.1 GI:13992531  
KEYWORDS KIAA0298 gene; L27a gene; ribosomal protein L27a; St5 gene gene;

SOURCE

Suppression of tumorigenicity 5.  
house mouse.  
Mus musculus

REFERENCE 1 (bases 1 to 202748)  
AUTHORS Amid, C., Hankeln, T., Winterpacht, A., Zabel, B. and Schmidt, E.  
JOURNML Unpublished  
REFERENCE 2 (bases 1 to 202748)  
AUTHORS Hankeln, T.  
TITLE Direct Submission  
JOURNML Submitted (04-MAY-2001) Hankeln T., Inst. Molekulargenet., Univ.  
Mainz, Becherweg 32, D-55099 Mainz, GERMANY  
FEATURES  
source Location/Qualifiers  
1..202748  
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/clone\_id="M1 Mouse Pl library"  
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110944..111013,113918..113995,114515..114655,  
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124609..125378)  
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31995..79182  
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121498..121675,121904..121945,122952..123063,  
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/db\_xref="GI:13992532"

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LAQSLSPSSPSSINEDLSSTSELSSRSRRIPKLVORINSITYNNAKGRKRLKLSM  
SLELTASLRDENSESDSDDRFAHQRLVRIQIOMLKRASPRSTLELELEWQERL  
FEYFVVVSLTKKPSRNTYLPVSYQFPKLRPPTKOMREAPERLKAIPQCFPPAKML  
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FIYVLPASMDIYCCPTPLVGLSSSLPKLELPEVLAALVMVNGSDFRQMDDEDT  
LTPKQALQALERKSELISODSDSDDECNLTNGLVSEVTRFREFVTGHSYSLF  
LTSEKGERAFORAPRKSVAASKSIRPFLFVPMESOMFAGFIODRELKCRANGLPEO  
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join(79208, 79287, 91832, 93082, 96174, 96310, 104057, 104208, 106750, 106965, 107853, 107949, 108849, 108893, 109439, 109662, 110242, 110351, 110944, 111013, 113918, 113995, 114515, 114655, 118059, 118207, 121498, 121675, 121904, 121945, 122952, 123063, 123511, 123750, 123940, 124026, 124609, 124643)  
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REFERENCE 1 (bases 1 to 64)  
AUTHORS Kufner,P., Zettl,F., Dreier,T., Baenerle,P.A. and Borschert,K.  
TITLE Heteromimibodies  
JOURNAL Patent: WO 0006605-A 13 10-FEB-2000;  
KUFNER PETER (DE) ; ZETTL FLORIAN (DE) ;  
BAENERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER  
BIOMEDIZINIS (DE)  
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BASE COUNT 15 a 15 c 22 g 12 t  
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Best Local Similarity 81.2%; Pred. No. 30;  
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Oy 1 gagctaccagtaacaaagcttaataagagagagtggtgagag 48  
||||| 11 11 11 11 11 11 11 11 11 11 11 11  
Db 4 GAGCTCGCCCGTCACAAAGAGCTTCAACAGGAGAGTGTGAGGTGC 51  
RESULT 5  
AL161896/c AL161896 96183 bp DNA PRI 20-JAN-2001  
LOCUS Human DNA sequence from clone RP11-261P24 on chromosome 13,  
DEFINITION complete sequence.  
ACCESSION AL161896  
VERSION AL161896.16 GI:12330752  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 96183)  
REFERENCE 1  
AUTHORS Phillimore,B.  
TITLE Direct Submission  
JOURNAL Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
COMMENT On Jan 22, 2001 this sequence version replaced gi:12329254.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence has been finished according to sequence map criteria  
as follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated repeat sequence elements. Where the sequence is  
ambiguous, there is an annotation using the 'unsure' feature key.  
The following abbreviations are used to associate primarily accession  
numbers given in the feature table with their source databases:  
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMEP; Information  
on the WORMEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 13, constructed by the Sanger Centre Chromosome 13  
Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr13  
RP11-261P24 is from the library RPC1-11.1 constructed by the group  
of Pister de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone  
RP11-261P24. It may be shorter because we sequence overlapping  
sections only once, except for a 100 base overlap.  
The true right end of clone RP11-261P24 is at 96183 in this  
sequence. The true left end of clone RP11-31K22 is at 59428 in this

sequence. The true right end of clone RP11-573N10 is at 100 in this  
sequence.  
FEATURES  
Source Location/Qualifiers  
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/note="MER20 repeat: matches 1..75 of consensus"  
repeat\_region 3518..3834  
/note="L1MB8 repeat: matches 5837..6173 of consensus"  
repeat\_region 5528..5599  
/note="12 copies 6 mer tatla 69% conserved"  
repeat\_region 5533..5604  
/note="36 copies 2 mer at 69% conserved"  
repeat\_region 5766..6068  
/note="AluSp repeat: matches 7..303 of consensus"  
repeat\_region 6949..7264  
/note="AluJo repeat: matches 1..307 of consensus"  
repeat\_region 7380..7503  
/note="MIR repeat: matches 65..191 of consensus"  
repeat\_region 8192..8407  
/note="L2 repeat: matches 2064..2289 of consensus"  
repeat\_region 8475..8506  
/note="16 copies 2 mer tt 100% conserved"  
repeat\_region 8929..9103  
/note="MER33 repeat: matches 4..171 of consensus"  
repeat\_region 9104..9421  
/note="AluJb repeat: matches 1..306 of consensus"  
repeat\_region 9422..9450  
/note="MER33 repeat: matches 171..216 of consensus"  
repeat\_region 9491..9595  
/note="MER33 repeat: matches 142..225 of consensus"  
repeat\_region 9596..9609  
/note="AluJ repeat: matches 1..311 of consensus"  
repeat\_region 9910..9997  
/note="MER33 repeat: matches 225..319 of consensus"  
repeat\_region 11665..11763  
/note="MIR repeat: matches 47..149 of consensus"  
repeat\_region 11991..12022  
/note="8 copies 4 mer tgtg 90% conserved"  
repeat\_region 12274..12568  
/note="AluX repeat: matches 20..311 of consensus"  
repeat\_region 12577..12879  
/note="AluY repeat: matches 1..304 of consensus"  
repeat\_region 13406..13549  
/note="MTR1C repeat: matches 1..146 of consensus"  
repeat\_region 13554..13585  
/note="16 copies 2 mer ca 96% conserved"  
repeat\_region 13682..13715  
/note="17 copies 2 mer ac 97% conserved"  
repeat\_region 13684..13715  
/note="8 copies 4 mer acac 100% conserved"  
repeat\_region 13752..13779  
/note="14 copies 2 mer ca 96% conserved"  
repeat\_region 13784..14048  
/note="MTR1C repeat: matches 189..465 of consensus"  
repeat\_region 14716..15018  
/note="AluSc repeat: matches 1..303 of consensus"  
repeat\_region 15567..15842  
/note="AluJo repeat: matches 3..305 of consensus"  
repeat\_region 16752..16916  
/note="MIR repeat: matches 63..227 of consensus"  
repeat\_region 17700..17838  
/note="AluJo/FRAM repeat: matches 163..301 of consensus"  
repeat\_region 18111..18314  
/note="MTR1A2 repeat: matches 157..359 of consensus"  
repeat\_region 18317..18428  
/note="28 copies 4 mer ctcc 71% conserved"

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repeat_region      18322..18423
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repeat_region      18510..18797
                    /note="Alu0 repeat: matches 1..302 of consensus"
repeat_region      18800..18956
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repeat_region      19392..19704
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repeat_region      28074..28174
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repeat_region      33871..33918
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repeat_region      33878..33921
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repeat_region      34367..34420
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Best Local Similarity 68.7%; Pred. No. 46;
Matches 46; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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RESULT      6
AC022669
LOCUS      Homo sapiens chromosome 15 clone RP11-96B23 map 15, WORKING DRAFT
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.

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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 152053)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckert,J., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Buxter,G., Castle,A.,
Choquel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArriano,K., Dewar,K., Domino,M., Doyle,M., Fenesor,J.,
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
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Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.

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TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 4, 2000 this sequence version replaced gi:7229803.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4938
Center clone name: 96-B-23
----- Summary Statistics
Sequencing vector: M13; M7815; 93% of reads

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Sequencing vector: Plasmid: n/a; %0.f%% of reads  
7.39091718610864Chemistry: Dye-terminator Big Dye; 100% of  
reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 136451 bases at least Q40  
Consensus quality: 143612 bases at least Q30  
Consensus quality: 146365 bases at least Q20  
Insert size: 158000; agarose-fp  
Insert size: 148853; sum-of-contigs  
Quality coverage: 3.4 in Q20 bases; agarose-fp  
Quality cov.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 33 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
785 884: gap of 100 bp  
885 1956: contig of 1072 bp in length  
1957 2056: gap of 100 bp  
2057 3113: contig of 1057 bp in length  
3114 3213: gap of 100 bp  
3214 4817: contig of 1604 bp in length  
4818 4917: gap of 100 bp  
4918 6582: contig of 1665 bp in length  
6583 8059: contig of 1377 bp in length  
8060 8159: gap of 100 bp  
8160 22369: contig of 14210 bp in length  
22370 22469: gap of 100 bp  
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24975 25074: gap of 100 bp  
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27207 27306: gap of 100 bp  
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29421 29520: gap of 100 bp  
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32001 32100: gap of 100 bp  
32101 36330: contig of 4230 bp in length  
36331 36430: gap of 100 bp  
36431 38067: contig of 2637 bp in length  
38068 39167: gap of 100 bp  
39168 42564: contig of 3397 bp in length  
42565 42664: gap of 100 bp  
42665 46664: contig of 4000 bp in length  
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51048 51147: gap of 100 bp  
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58832 58931: gap of 100 bp  
58932 64077: contig of 5146 bp in length  
64078 64177: gap of 100 bp  
64178 68808: contig of 4631 bp in length  
68809 68908: gap of 100 bp  
68909 74170: contig of 5262 bp in length  
74171 74270: gap of 100 bp  
74271 79296: contig of 5026 bp in length  
79297 79396: gap of 100 bp  
79397 84724: contig of 5328 bp in length  
84725 84824: gap of 100 bp  
84825 89713: contig of 4889 bp in length  
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89814 94721: contig of 4908 bp in length  
94722 94821: gap of 100 bp  
94822 100196: contig of 5375 bp in length  
100197 100296: gap of 100 bp  
100297 107015: contig of 6719 bp in length  
107016 107115: gap of 100 bp

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\* 114508 114607: gap of 100 bp  
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\* 122672 122771: gap of 100 bp  
\* 122772 128052: contig of 5281 bp in length  
\* 128053 128152: gap of 100 bp  
\* 128153 138583: contig of 10431 bp in length  
\* 138584 138683: gap of 100 bp  
\* 138684 150248: contig of 11565 bp in length  
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Matches 46; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Db 54558 AGATTCGACGTAGAAATAATTCTCCGCTCGGCAACTGTGAAGAAGAAAAGAAATTAA 54517

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Db 54518 TAATACT 54524

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DEFINITION   Arabidopsis thaliana genomic DNA, chromosome 5, pl clone:MXM12.
ACCESSION    AB005249 BA000015
VERSION      AB005249.1 GI:2264321
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ORGANISM     Arabidopsis thaliana (strain:Columbia) DNA, clone_11b:Mitsui PJ
              clone:MXM12.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (sites)
Sato,S., Kotani,H., Nakamura,Y., Kaneko,T., Asamizu,E., Fukami,M.,
Miyaizima,N. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. I.
Sequence features of the 1.6 Mb regions covered by twenty
physically assigned P1 clones
DNA Res. 4 (3), 215-230 (1997)
97471969
2 (bases 1 to 83599)
Nakamura,Y.
Direct Submission
Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yinakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MXM12
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Zolker Brendel, Stanford University,
http://gremiln1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-se/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
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TFIDSEWYLDQLSAHHNTRKVCROTLYVGGFVGLERGTVPNPDIYSALLHRLK  
KGVLAVOGTDRPQQLRVYAHCSGRAGVTLILINSQSDFTVSNGINVLNLSRK  
KKSLLDPLKRFPSWIGSKASDGLNREBYHLTPENGVLRSKTVLNGSKSLKPTATGDI  
PSLEPVLRSVSPNLVPLSMSTVFLPFDASACS"  
complement(129080..29607)  
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/codon\_start=1  
/evidence=not\_experimental  
/protein\_id="BAB09948.1"  
/db\_xref="GI:10176718"  
/translation="MLOBQVALSFRNSFRRRSMETGVDRDDGMQTLHKAEGUL  
KAVVELLDQADVALACGPKSGMTPLHLAKGHIENVMDLLERANEARISGAC  
GWPLHLAAAKERREAVKFLVNGAFLPDDITDSRNPVQYCHGLEWAYEERKLS  
DTLSGCDTSCDSAN"  
join(31233..31706,31923..32819)  
/note="gene\_id:MMJ2.9"  
/codon\_start=1  
/evidence=not\_experimental  
/product="anthranilate  
N-hydroxycinnamoyl/benzoyl transferase-like protein"  
/protein\_id="BAB09949.1"  
/db\_xref="GI:10176719"

Qy	3	gctcaccgtacaagaagcttaagagagagtgtagaggaagaadaaatgaag	62	/translation="MDSSTSEKRVYSCFVAPKRTIPPEKMKRPHILSPDLVMSMHL ONGLFLKSDATNTKDMETWLOKLRSLAEITLVHFFPLAGRLSTLKTDPNRSYSVF
Db	6199	GTTTAAAGAAAAACCACTTAACACAGATTGTTGATTCACAAAAAAGAAAG	6140	
Qy	63	aaac	67	
Db	6139	AAAC	6135	
RESULT	8			
LOCUS	HS11M5	107526 bp	DNA	PRI 23-NOV-1999
DEFINITION	Human DNA sequence from PAC 11M5 on chromosome 6. Contains BBCT1, RFP finger protein, EST, STS, tRNAs and polymorphic repeat.			
ACCESSION	Z84474			
VERSION	284474.1	GI:1903188		
KEYWORDS	6p21.3; BBCT1; repeat polymorphism; RFP transforming protein.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Mallett,D.			
TITLE	Direct Submission			
JOURNAL	Submitted (11-MAR-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. Chromosome 6 Project Group (http://www.sanger.ac.uk/chr6/); E-mail enquiries: hunquyer@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Mar 21, 1997 this sequence version replaced g1:1806002. de Jong P.J., enquires: http://bacpac.med.buffalo.edu/ IMPORTANT: This sequence is the entire insert of clone 11M5. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 11M5 is at 1 in this sequence. The true right end of clone 11M5 is at 107526. 11M5 is from the human PAC library described in Ioannou A.P. et al Nature Genet 6, 84-89.			
COMMENT	Location/Qualifiers 1..107526 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="6p21.3" /clone.lib="RPC1-1" /clone="RPI-11M5" 597..874 /note="Alusg repeat: matches 300..1 of consensus" 941..1225 /note="Alusx repeat: matches 2..299 of consensus" 1264..1376 /note="Alusc repeat: matches 297..177 of consensus; incomplete repeat" 1648..1929 /note="Alusq repeat: matches 2..283 of consensus; incomplete repeat" complement(4210..4281) /note="Ala-tRNA" 5042..5329 /note="Alusx repeat: matches 1..294 of consensus" 5332..5581 /note="MER42c repeat: matches 178..432 of consensus" 5584..5877			

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repeat_region /note="AluSx repeat: matches 8. .302 of consensus"  
5939. .6045  
/note="MER42c repeat: matches 1432. .138 of consensus"  
repeat_region 7653. 7968  
/note="MER5A repeat: matches 189. .73 of consensus"  
/note="Ala-tRNA"  
9923. .10061  
/note="AluJ repeat: matches 134. .273 of consensus;  
incomplete repeat"  
repeat_region 10072. .10131  
/note="6 copies of 10 mer 83 % conserved"  
11296. .11407  
/note="MER33 repeat: matches 1. .114 of consensus"  
repeat_region 11413. .11712  
/note="AluSg repeat: matches 290. .1 of consensus"  
11733. .11825  
/note="MER33 repeat: matches 132. .228 of consensus"  
repeat_region 11812. .12027  
/note="L1PA16 repeat: matches 685. .904 of consensus"  
12043. .12329  
/note="AluSx repeat: matches 292. .6 of consensus"  
12348. .12448  
/note="MER33 repeat: matches 203. .313 of consensus"  
12843. .13179  
/note="AluYb8 repeat: matches 306. .1 of consensus"  
13621. .13920  
/note="AluSg repeat: matches 1. .300 of consensus"  
14058. .14366  
/note="AluJ repeat: matches 1. .294 of consensus"  
14370. .14661  
/note="AluY repeat: matches 1. .293 of consensus"  
14725. .15015  
/note="AluY repeat: matches 301. .1 of consensus"  
complement(15454. .15527)  
/note="Phe-tRNA"  
15739. .16038  
/note="AluSx repeat: matches 1. .302 of consensus"  
16634. .16730  
/note="AluSc repeat: matches 279. .177 of consensus;  
incomplete repeat"  
18918. .19219  
/note="AluSp repeat: matches 1. .302 of consensus"  
19849. .20487  
/note="L1MC3 repeat: matches 1000. .1666 of consensus"  
20025. .20622  
/note="MER42c repeat: matches 2. .664 of consensus"  
20623. .20754  
/note="AluSp repeat: matches 1. .132 of consensus;  
incomplete repeat"  
20756. .20838  
/note="AluSp repeat: matches 221. .303 of consensus;  
incomplete repeat"  
20844. .20967  
/note="MER42c repeat: matches 876. .1007 of consensus"  
20898. .21332  
/note="MER42c repeat: matches 950. .1414 of consensus"  
21340. .21363  
/note="12 copies of 2 mer 96 % conserved"  
21544. .21844  
/note="AluSp repeat: matches 301. .1 of consensus"  
21845. .21925  
/note="MER7B repeat: matches 1125. .1205 of consensus"  
21927. .22031  
/note="L1 repeat: matches 398. .502 of consensus"  
22120. .23607  
/note="L1 repeat: matches 3912. .5390 of consensus"  
23448. .24371  
/note="L1PA2 repeat: matches 1. .891 of consensus"  
24401. .24712  
/note="AluY repeat: matches 1. .301 of consensus"  
25006. .25306  
/note="AluSx repeat: matches 1. .302 of consensus"  
  
repeat_region 26625. .26937  
/note="AluY repeat: matches 1. .301 of consensus"  
27763. .27935  
/note="AluSg repeat: matches 298. .126 of consensus;  
incomplete repeat"  
28981. .29275  
/note="AluSg repeat: matches 1. .300 of consensus"  
29517. .29623  
/note="MER5A repeat: matches 175. .45 of consensus"  
29962. .30257  
/note="AluY repeat: matches 1. .301 of consensus"  
complement(30589. .30660)  
/note="Ala-tRNA"  
32596. .32733  
/note="L1 repeat: matches 3715. .3849 of consensus"  
32741. .32961  
/note="L1MA4A repeat: matches 599. .815 of consensus"  
32962. .33152  
/note="AluSg repeat: matches 300. .107 of consensus;  
incomplete repeat"  
33153. .33277  
/note="L1MA4A repeat: matches 839. .967 of consensus"  
33320. .33462  
/note="L1ME1 repeat: matches 244. .387 of consensus"  
33500. .33800  
/note="AluSx repeat: matches 1. .300 of consensus"  
33886. .34143  
/note="AluY repeat: matches 1. .301 of consensus"  
34146. .34226  
/note="L1MD2 repeat: matches 479. .570 of consensus"  
34270. .34433  
/note="MER34 repeat: matches 181. .14 of consensus"  
34694. .34996  
/note="AluSx repeat: matches 2. .302 of consensus"  
35647. .35949  
/note="AluY repeat: matches 1. .300 of consensus"  
35959. .36155  
/note="AluY repeat: matches 3940. .4146 of consensus"  
36165. .36455  
/note="AluJ repeat: matches 7. .300 of consensus"  
36468. .37095  
/note="L1 repeat: matches 4143. .4754 of consensus"  
37106. .37405  
/note="AluSg repeat: matches 1. .292 of consensus"  
37415. .38029  
/note="L1 repeat: matches 4763. .5390 of consensus"  
37879. .38207  
/note="L1PA15 repeat: matches 2. .330 of consensus"  
38254. .38510  
/note="MER21A repeat: matches 907. .665 of consensus"  
38481. .38957  
/note="MER21B repeat: matches 521. .1 of consensus"  
38622. .39015  
/note="MER21A repeat: matches 416. .6 of consensus"  
39007. .39589  
/note="L1MB2 repeat: matches 323. .914 of consensus"  
39624. .39914  
/note="AluSx repeat: matches 2. .296 of consensus"  
39919. .40259  
/note="L1 repeat: matches 2937. .3293 of consensus"  
40273. .40549  
/note="AluSg repeat: matches 5. .298 of consensus"  
40588. .42050  
/note="L1 repeat: matches 5. .1449 of consensus"  
42051. .42350  
/note="AluY repeat: matches 2. .301 of consensus"  
42352. .46319  
/note="L1 repeat: matches 1430. .5390 of consensus"  
46170. .47057  
/note="L1PA2 repeat: matches 1. .892 of consensus"  
47151. .47452  
/note="AluSx repeat: matches 301. .1 of consensus"
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[illegible]

requests: clonerequests@sanger.ac.uk

On Jun 27, 2001 this sequence version replaced gi:14270608.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone, and the abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, SW., SWISSPROT, Tr., TREMBL, Wp., WORMPEP; information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>

RP11-477J21 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see

<http://www.choi1.org/bacpac/home.htm>

VECTOR: PBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-477J21. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP11-477J21 is at 108930. In this sequence. The true left end of clone RP11-342H3 is at 23985. In this sequence. The true right end of clone RP11-165P4 is at 100 in this sequence.

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FEATURES             location/Qualifiers
    source            1..108930
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                        /db_xref="taxon:9606"
                        /chromosome="9"
                        /clone="RP11-477J21"
                        /clone.lib="RPCI-11.2"
                        1..187
repeat_1region       /note="MER21B repeat: matches 6..201 of consensus"
                        605..725
repeat_2region       /note="12 repeat: matches 2624..2746 of consensus"
                        879..1178
repeat_3region       /note="Aluub repeat: matches 1..309 of consensus"
                        1187..1672
repeat_4region       /note="LIMC4 repeat: matches 7492..7975 of consensus"
                        1673..1972
repeat_5region       /note="AluSx repeat: matches 1..304 of consensus"
                        1973..2675
repeat_6region       /note="LIMC4 repeat: matches 6783..7492 of consensus"
                        3053..3202
repeat_7region       /note="MIR repeat: matches 82..248 of consensus"
                        4252..4523
repeat_8region       /note="AluSg repeat: matches 1..283 of consensus"
                        4641..4753
repeat_9region       /note="12 repeat: matches 2589..2710 of consensus"
                        5008..5134
repeat_10region      /note="L1MB1 repeat: matches 6042..6168 of consensus"
                        5296..5413
repeat_11region      /note="HERVL repeat: matches 4908..5022 of consensus"
                        5414..5637
repeat_12region      /note="MIR1G repeat: matches 1..216 of consensus"
                        5638..5940
repeat_13region      /note="AluSg repeat: matches 1..302 of consensus"
                        5941..6209
repeat_14region      /note="MIR1G repeat: matches 216..510 of consensus"
                        6210..6337
repeat_15region      /note="HERVL repeat: matches 4794..4908 of consensus"
                        6328..6781

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```

/note="MLT1J repeat: matches 1. .516 of consensus"
6782. .7153
repeat_region
/note="HRRVL repeat: matches 4402. .4794 of consensus"
7157. .7314
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/note="FRAM repeat: matches 1. .158 of consensus"
8178. .8363
repeat_region
/note="MLT1J repeat: matches 1. .200 of consensus"
8396. .8634
repeat_region
/note="MLT1C repeat: matches 220. .466 of consensus"
8664. .8966
repeat_region
/note="AluSg repeat: matches 1. .308 of consensus"
9734. .10026
repeat_region
/note="AluYb repeat: matches 1. .304 of consensus"
10611. .11123
repeat_region
/note="MLT2B repeat: matches 1. .448 of consensus"
125451. .12786
repeat_region
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13425. .13855
repeat_region
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13905. .14075
repeat_region
/note="MIR repeat: matches 50. .216 of consensus"
14560. .14653
repeat_region
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15446. .15938
repeat_region
/note="MLT1D repeat: matches 1. .502 of consensus"
16000. .16056
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/note="LIME1 repeat: matches 6105. .6162 of consensus"
16057. .26331
repeat_region
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repeat_region
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17803. .18108
repeat_region
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18212. .18370
repeat_region
/note="FAM repeat: matches 1. .159 of consensus"
18400. .18716
repeat_region
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20637. .20795
repeat_region
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20939. .21587
repeat_region
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21634. .21947
repeat_region
/note="AluYb repeat: matches 1. .299 of consensus"
22652. .22956
repeat_region
/note="AluSg repeat: matches 1. .305 of consensus"
23007. .23286
repeat_region
/note="AluSg repeat: matches 5. .283 of consensus"
23327. .23364
repeat_region
/note="L9 copies 2 mer gt 100% conserved"
23383. .23579
repeat_region
/note="AluYb repeat: matches 1. .193 of consensus"
23639. .23950
repeat_region
/note="AluSx repeat: matches 1. .298 of consensus"
24131. .24437
repeat_region
/note="AluSg repeat: matches 1. .305 of consensus"
24478. .24527
repeat_region
/note="L2 repeat: matches 2698. .2747 of consensus"
24643. .24880
repeat_region
/note="L2 repeat: matches 2248. .2476 of consensus"
24954. .25299
repeat_region
/note="MLT1 repeat: matches 68. .410 of consensus"
25300. .25344
repeat_region
/note="L2 repeat: matches 2197. .2235 of consensus"
25345. .25707
repeat_region
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25708. .25752
repeat_region
/note="L2 repeat: matches 2151. .2197 of consensus"
27394. .27701
repeat_region
/note="AluY repeat: matches 1. .309 of consensus"
27703. .27989
repeat_region
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repeat_region 28758. .29049
/note="LIMA4 repeat: matches 5769. .6074 of consensus"
repeat_region 29050. .29372
/note="AluSg repeat: matches 1. .311 of consensus"
repeat_region 29373. .29603
/note="LIMA4 repeat: matches 6074. .6300 of consensus"
repeat_region 29698. .29949
/note="MIR repeat: matches 12. .262 of consensus"
repeat_region 29964. .30044
/note="MIR repeat: matches 127. .197 of consensus"
repeat_region 30045. .30356
/note="AluSx repeat: matches 3. .312 of consensus"
repeat_region 30357. .30390
/note="MIR repeat: matches 92. .127 of consensus"
repeat_region 30668. .30932
/note="AluSx repeat: matches 40. .298 of consensus"
repeat_region 31360. .31519
/note="L2 repeat: matches 2540. .2710 of consensus"
repeat_region 31530. .31778
/note="L2 repeat: matches 2483. .2746 of consensus"
repeat_region 31834. .32101
/note="L2 repeat: matches 2243. .2508 of consensus"
repeat_region 33093. .33156
/note="MIR repeat: matches 86. .151 of consensus"
repeat_region 33878. .34052
/note="MIR repeat: matches 20. .199 of consensus"
repeat_region 34281. .34362
/note="MIR repeat: matches 98. .194 of consensus"
repeat_region 34707. .34926
/note="MIR repeat: matches 20. .262 of consensus"
repeat_region 35373. .35551
/note="L2 repeat: matches 2520. .2710 of consensus"
repeat_region 35560. .35847
/note="MER63B repeat: matches 1. .278 of consensus"
repeat_region 35848. .36062
/note="THE1C repeat: matches 166. .371 of consensus"
repeat_region 36063. .36363

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Query Match 39.8%; Score 32.2; DB 9; Length 108930;  
 Best Local Similarity 66.7%; Pred. No. 94;  
 Matches 46; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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QY 12 taacaaagcttaatagaggagagtgctgagggagaaaaaatgaagaaactgct 71
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9499 TGACTAAATCATTAATAGAGTGTCTTGCGGTACACAAAGAAAGAAACACT 9440

QY 72 atagcaatt 80
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9439 ATAGCAATT 9431

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RESULT 12  
 AP003340  
 LOCUS Oryza sativa chromosome 1 clone OJ1316\_H05, \*\*\* SEQUENCING IN DEFINITION  
 AP003340  
 VERSION HTG: HTGS PHASE2  
 KEYWORDS Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1316\_H05.  
 SOURCE Oryza sativa  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (sites)  
 REFERENCES  
 Sasaki,T., Matsumoto,T. and Yamamoto,K.  
 Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OJ1316\_H05  
 JOURNAL Published Only in DataBase (2001) In press  
 REFERENCE 2 (bases 1 to 109422)  
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE	Direct Submission
JOURNAL	Submitted (28-FEB-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakia@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
COMMENT	
FEATURES	
source	Location/Qualifiers 1..109422 /organism="Oryza sativa" /cultivar="Nipponbare" /db_xref="taxon:4530" /chromosome="1" /clone="OJ131_H05"
BASE COUNT	30559 a 23093 c 23374 g 32146 t 250 others
ORIGIN	
Query Match	39.8%; Score 32.2; DB 2; Length 109422;
Best Local Similarity	63.6%; Pred. No. 94;
Matches 49; Conservativ	0; Mismatches 28; Indels 0; Gaps 0;
OY	4 CTCACCAGTAACTAACAAGCCTTAATGAGGAGAGTCGTGAGGAGGAAAAAATCGAAGA 63                                                                   Db 102204 CTCAGAACATCATGAAGGAGGAGTGCTGTAGAAAGTTGAGAGAAAAGAGAAA 102263
Oy	64 aaacgtctatgcaatt 80 
Db 102264	AGTAGCTATGACTATT 102280
RESULT 13	
LOCUS	AP003792/c
DEFINITION	AP003792 150380 bp DNA HTG 28-JUN-2001
ACCESSION	Oryza sativa chromosome 1 clone OJ1159_D09, *** SEQUENCING IN
VERSION	PROGRESS ***, In ordered pieces.
KEYWORDS	AP003792
SOURCE	AP003792.1 GI:14572677
ORGANISM	HTG: HTGS.PHASE2.
REFERENCE	Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1159_D09.
AUTHORS	Oryza sativa
TITLE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehretoidaeae; Oryzaceae; Oryza.
COMMENT	1 (sites) Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OJ1159_D09 Published Only in Database (2001) In press 2 (bases 1 to 150380) Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission submitted (27-JUN-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kamondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakia@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data. NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them

FEATURES	source
BASE COUNT	41983 a 33202 c 32862 g 42033 t 300 others
ORIGIN	<pre> 1..150380    /organism="Oryza sativa"    /cultivar="Nipponbare"    /db_xref="taxon:4530"    /chromosome="1"    /clone="OJ1159_009" </pre>
Query Match	39.8% Score 32.2; DB 2; Length 150380; +
Best Local Similarity	63.6% Pred. No. 95;
Matches 49; Conservative 0; Mismatches 28; Indels 0; Gaps 0;	
QY 4	ctccaccgtacaaaagctttaagagagagtggtgagagagaaaaaatgtaaga 63
Db 145440	CTCAGAAACACTGTGAGAGGTGGAGCTGTGAAAGTTGAAGAAAAAAGGAAA 145381
QY 64	aaactgctatagcaatt 80
Db 145380	AGTATGCTATAGCATTT 145364
RESULT 14	
AC006558/c	
LOCUS	AC006558 207392 bp DNA HTG 10-FEB-1999
DEFINITION	Homo sapiens chromosome 9 clone hRPK.477_J_21 map 9, *** SEQUENCING
ACCESSION	AC006558
VERSION	AC006558.1 GI:4262259
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 207392)
JOURNAL	Birren,B., Linton,L., Nusbaum,C. and Lander,E.
REFERENCE	Homo sapiens chromosome 9, clone hRPK.477_J_21
AUTHORS	Unpublished
	2 (bases 1 to 207392)
	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
	Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
	Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
	Cooke,P., Dearellano,K., Depuyre,E., Devon,K., Dewar,K.,
	Donelan,J., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C.,
	Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,
	Hagos,A., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
	Karasas,A., Leacock,J., Liu,C., Locke,K., Macdonald,P.,
	Marguis,N., McEwan,P., McGurt,A., McKernan,K., McLaughlin,J.,
	Meidrum,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,B.,
	Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
	Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
	Strange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
	Teefie,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
	Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
	Direct Submission
	Submitted (10-FEB-1999) Whitehead Institute/MIT Center for Genome
	Research, 320 Charles Street, Cambridge, MA 02141, USA
	All repeats were identified using RepeatMasker: Smit, A.F.A. &
	Green, P. (1996-1997)
	<a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a> .
	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 7 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:49:56 ; Search time 230.28 Seconds  
(without alignments)  
301.560 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 1 gagctccaccgtaacacaaa.....gaaacgtctatagcaattg 81

Sequence: 1 gagctccaccgtaacacaaa.....gaaacgtctatagcaattg 81

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq.1101.\*

- 1: /SIDSR/gcgdata/geneseq/geneseqn/NA1980.DAT.\*
- 2: /SIDSR/gcgdata/geneseq/geneseqn/NA1981.DAT.\*
- 3: /SIDSR/gcgdata/geneseq/geneseqn/NA1982.DAT.\*
- 4: /SIDSR/gcgdata/geneseq/geneseqn/NA1983.DAT.\*
- 5: /SIDSR/gcgdata/geneseq/geneseqn/NA1984.DAT.\*
- 6: /SIDSR/gcgdata/geneseq/geneseqn/NA1985.DAT.\*
- 7: /SIDSR/gcgdata/geneseq/geneseqn/NA1986.DAT.\*
- 8: /SIDSR/gcgdata/geneseq/geneseqn/NA1987.DAT.\*
- 9: /SIDSR/gcgdata/geneseq/geneseqn/NA1988.DAT.\*
- 10: /SIDSR/gcgdata/geneseq/geneseqn/NA1989.DAT.\*
- 11: /SIDSR/gcgdata/geneseq/geneseqn/NA1990.DAT.\*
- 12: /SIDSR/gcgdata/geneseq/geneseqn/NA1991.DAT.\*
- 13: /SIDSR/gcgdata/geneseq/geneseqn/NA1992.DAT.\*
- 14: /SIDSR/gcgdata/geneseq/geneseqn/NA1993.DAT.\*
- 15: /SIDSR/gcgdata/geneseq/geneseqn/NA1994.DAT.\*
- 16: /SIDSR/gcgdata/geneseq/geneseqn/NA1995.DAT.\*
- 17: /SIDSR/gcgdata/geneseq/geneseqn/NA1996.DAT.\*
- 18: /SIDSR/gcgdata/geneseq/geneseqn/NA1997.DAT.\*
- 19: /SIDSR/gcgdata/geneseq/geneseqn/NA1998.DAT.\*
- 20: /SIDSR/gcgdata/geneseq/geneseqn/NA1999.DAT.\*
- 21: /SIDSR/gcgdata/geneseq/geneseqn/NA2000.DAT.\*
- 22: /SIDSR/gcgdata/geneseq/geneseqn/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.2	63.2	66	20	AAK55755
2	35.2	43.5	1630	21	AAZ50588
3	33.6	41.5	64	21	AAZ50601
4	32.8	40.5	548	16	AAZ23297
5	32	39.5	4691	16	AAO92546
6	32	39.5	5924	21	AAZ38921
7	32	39.5	5925	21	AAZ38770
8	32	39.5	6166	16	AAO92547
9	31.8	39.3	705	18	AAAT61240
10	31.8	39.3	708	18	AAAT61242
11	31.8	39.3	708	21	AAA63530

12	31.8	39.3	720	18	AAAT62511	Primate anti-hu
13	31.8	39.3	720	19	AAV35486	Macaque primatized
14	31.8	39.3	725	20	AAZ22287	Nucleotide sequenc
15	31.8	39.3	6709	22	AAZ30339	Bicistronic plasmid
16	31.8	39.3	7521	22	AAZ30315	Bicistronic chimera
17	31.8	39.3	8540	15	AAO65628	Vector contig. TCAE
18	31.8	39.3	9208	15	AAO65629	Vector contig. TCAE
19	31.8	39.3	19001	19	AAZ61793	Traget plasmid Mol
20	31.8	39.3	19035	19	AAZ61794	Traget plasmid Mol
21	31.4	38.8	111	14	AAO48067	Human kappa light
22	31.4	38.8	117	14	AAO48067	Human kappa light
23	31.4	38.8	724	20	AAZ90423	Chimeric antibody
24	31.4	38.8	3169	17	AAZ8397	Price 99 plasmid fr
25	31.2	38.5	779	21	AAZ87973	Humanised anti-IL-
26	31.2	38.5	780	19	AAV55070	Humanised anti-IL-
27	31.2	38.5	780	19	AAV55071	Humanised anti-IL-
28	31.2	38.5	780	20	AAZ90541	Humanised anti-IL-
29	31.2	38.5	780	20	AAZ90542	Anti-human-IL-8 6G
30	31.2	38.5	780	20	AAZ90577	Humanised anti-IL-
31	31.2	38.5	780	21	AAZ65506	6G4-2-VY11 light c
32	31.2	38.5	780	21	AAZ65507	GCN4 leucine zipper
33	31.2	38.5	780	21	AAZ87967	Humanised anti-IL-
34	31.2	38.5	780	21	AAZ87967	Humanised anti-IL-
35	31.2	38.5	780	21	AAZ87968	Humanised anti-IL-
36	31.2	38.5	1493	20	AAZ07423	PS1130 expression
37	31.2	38.5	2143	20	AAZ03840	Plasmid pS1130 exp
38	31.2	38.5	2143	21	AAZ53339	Expression cassett
39	31.2	38.5	2143	22	AAZ31463	ps 1130 expression
40	31.2	38.5	2178	13	AAQ25592	Encodes 405 Fab Ig
41	31.2	38.5	2178	20	AAZ81689	4D5 Fab molecule e
42	31.2	38.5	6072	19	AAZ71266	VEGF humanised ant
43	31.2	38.5	6072	19	AAZ63493	Rab-display antio
44	31.2	38.5	6127	20	AAZ07474	Mus musculus anti-
45	31.2	38.5	6127	22	AAZ69253	Expression plasmid

# ALIGNMENTS

RESULT	1
ID	AAK55755 standard; DNA; 66 BP.
AC	AAK55755;
XX	
DT	30-JUL-1999 (first entry)
XX	
DE	PCR mutagenic oligo.
XX	
KW	Hinge peptide; cell-associated receptor; dimeric antibody; medicine;
KW	Infectious disease; inflammatory disease; autoimmunity; osteoarthritis;
KW	Allergy; atopic disease; asthma; congenital disease; cystic fibrosis;
KW	Dermatological disease; psoriasis; neurological; metabolic; cancer;
KW	PCR primer; mutagenic; ss.
XX	
OS	Synthetic.
XX	
PN	WO915549-A2.
XX	
PD	01-APR-1999.
XX	
PE	21-SEP-1998; 98WO-G02851.
XX	
PR	19-SEP-1997; 97GB-0020054.
XX	
PA	(CIAT ) CELLTECH THERAPEUTICS LTD.
XX	
PI	Humphreys DP;
XX	
XX	
DR	WPI; 1999-244365/20.
XX	
PT	New peptides, useful as hinge regions in proteins for producing
PT	dimeric proteins for use in therapy

XX Example 1; Page 13; 47ppi English.  
PS

The invention relates to a peptide of 14 defined amino acids which functions as a hinge region in proteins. The peptide has formula (I):  $\text{MTCPCPCXXCPCPCPC}$ , where X and Y are neutral aliphatic L-amino acid residues. The new peptide is useful as a hinge region in proteins, especially cell-associated receptors or dimeric antibodies, which are useful in medicine. The new peptides are useful for replacing naturally occurring hinge regions. The proteins are useful for diagnosis and/or treatment of diseases or disorders including infectious diseases; inflammatory disease/ autoimmunity e.g. cancer, osteoarthritis; allergic/atopic disease e.g. asthma; congenital disease e.g. cystic fibrosis; dermatological disease e.g. psoriasis; neurological disease and metabolic diseases. The new peptide allows production of divalent antigen binding species e.g. dimeric antibodies, which are non-immunogenic, are not easily cleaved *in vivo*, are easy to prepare recombinantly and can couple to other effector proteins.

.....  
SQ Sequence 66 BP; 28 A; 9 C; 18 G; 11 T; 0 other;

Query Match	63.2%	Score	51.2	DB 20,	Length	66;			
Best Local Similarity	94.6%	Pred. No.	1.1e-05;						
Matches	53;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;

Qy 1 gagctcaccagtaacaaaaagctttaatagagagagtgcttgaggagaaaaaaa 56  
 |||||  
 6 gagctcaccagtaacaaaaagctttaatagagagagtgcttgaggagaaaaaaa 61

## RESULT 2

ID AAZ50588 standard; DNA; 1630 BP.

AC AAZ50588;

DT 23-MAY-2000 (first entry)

DE HD70scFv-Ck-interleukin 2 encoding DNA

KM H270: single-chain variable fragment; scFv; 17-1A antigen; human;  
 KM E5C4M: epithelial cell adhesion molecule; inflammatory cytokine;  
 KM IL-2: interleukin-2; Cx-domain; kappa light chain constant domain;  
 KM haemochromin; multifunctional compound; immunoglobulin;  
 KM cytosolic; immunostimulatory; anti-leukemia; diagnosis; prevention;  
 KM antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KM leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.

OS Homo sapiens

Key	Location/Qualifiers
EH	39..1613
FT	/*tag= a
FT	/*product= "HD70scfv-ck-IL-2 chain"
FT	96..842
FT	/*tag= b
FT	/*label= HD70_scfv

PN WO200006605-A2.

PD 10-FEB-2000.

PF 28-JUL-1999; 99WO-EP05416.

PR 28-JUL-1998; 98EP-0114082.

PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.

PI Kufer P, Dreier T, Baueerle PA, Borschert K, Zettl F,

DR WPI; 2000-195265/17.

1000

xx New multifunctional compounds useful for preventing and/or treating  
 pt malignant cell growth and for detection and diagnosis -  
 pr  
 xx  
 ps Claim 8; Fig 55B; 166pp; English.

The patent discloses heteroantibodies which are multifunctional compounds producible in a mammalian host cell as a secretable and fully functional heterodimer of two polypeptide chains, where one of the polypeptide chains comprises, a CH1-domain (constant domain of an immunoglobulin heavy chain) and the other chain comprises CL-domain (constant domain of an immunoglobulin light chain). The polypeptide chains further comprise, fused to the constant domains at least two (polypeptides having different receptor or ligand functions, where further at least two of the different (polypeptides lack an intrinsic affinity for one another and are linked via the constant domains. The heteroantibodies have cytostatic, immunostimulatory, antileukaemia and antiproliferative activities. These compounds can be used for diagnosing, preventing and treating malignant cell growth related to malignancies of hematopoietic cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas, melanomas and sarcomas.

The present sequence is a DNA encoding right chain of a heteroantibody comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to human Cκ domain (constant domain of immunoglobulin kappa light chain) which bears at its C-terminus the human inflammatory cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen.

Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 other;

Query Match 43.58; Score 35.2; DB 21; Length 1630;

```
Matches 40; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

QY	1	gagctcaccagtaacaaaaagcttataagagagagtgttagagag	48
Db	1154	gagctcgcccgtaacaaagagcttcaacagaggagagatgttcagagag	1201

## RESULT

ID AA250601 standard; DNA; 64 BP.

AC AAZ50601;

DT 23-MAY-2000 (first entry)

DE 5' VHTR66CKSAC primer to obtain anti-CD3 antibody TR66 scFv-fragment.

KW CD3; TR6; antibody; scFv; single-chain Fv; fragment; M79; 17-1A antigen;  
 KW heronemithbody; multifunctional compound; immunoglobulin; prevention;  
 KW cycostatic; immunostimulatory; antileukaemia; diagnosis; constant domain;  
 KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
 KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; PCR primer; ss.  
 XX Unidentified.

PN WO200006605-A2

PD 10-FEB-2000.

PF 28-JUL-1999

PR 28-JUL-1998; 98EP-0114082.

PA (MICR-) MICROMET GES BIOMEDI

PI Kufer P, Dreier T, Baeuerle PA, Borschert K,

DR WPI; 2000-195265/17

PT New multifunctional compounds useful for preventing and/or treating



PT malignant cell growth and for detection and diagnosis -  
 XX  
 PS Example 7; Page 67; 166pp; English.  
 XX  
 CC The patent discloses heteroantibodies which are multifunctional compounds  
 CC producible in a mammalian host cell as a secretable and fully functional  
 CC heterodimer of two polypeptide chains, where one of the polypeptide  
 CC chains comprises a CH1-domain (constant domain of an immunoglobulin  
 CC heavy chain) and the other chain comprises C $\mu$ -domain (constant domain of  
 CC an immunoglobulin light chain). The polypeptide chains further comprise,  
 CC fused to the constant domains at least two (polypeptides having  
 CC different receptor of ligand functions, where further at least two of the  
 CC different (poly)peptides lack an intrinsic affinity for one another and  
 CC are linked via the constant domains. The heteroantibodies have  
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
 CC activities. These compounds can be used for diagnosing, preventing and  
 CC treating malignant cell growth related to malignancies of haematopoietic  
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
 CC melanomas and sarcomas.  
 CC The present sequence is a 5' VHR66CKSAC primer used to amplify  
 CC the antiCD3scfv-fragment (single-chain Fv fragment) from the DNA  
 CC encoding bispecific single chain antibody M79scfv-antiCD3scfv.  
 CC The antiCD3scfv-fragment is used in the construction of a heteroantibody  
 CC M79scfvKantiCD3scfv/CD80CH1 comprising the single-chain Fv fragment of  
 CC murine anti 17-1A antibody M79, the constant domains of human IgG1 heavy  
 CC chain and kappa light chain, and CD80 molecule. The primer also  
 CC introduces a restriction cleavage site SacI.  
 CC  
 XX  
 SQ Sequence 64 BP; 15 A; 15 C; 22 G; 12 T; 0 other;  
 Query Match 41.5%; Score 33.6; DB 21; Length 64;  
 Best Local Similarity 81.2%; Pred. No. 0.77;  
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Oy 1 gagctaccagctaacaaaagcttaataagagagagtggtgagagag 48  
 Db 4 gagctgcgcgcgtcaccaagagcttcacacagggagagtggtgagag 51  
 RESULT 4  
 AAT23297  
 ID AAT23297 standard; cDNA to mRNA; 548 BP.  
 XX  
 AC AAT23297;  
 XX  
 DT 30-AUG-1996 (first entry)  
 XX  
 DE Human gene signature HUMGS05111.  
 XX  
 KW Gene signature: messenger RNA; mRNA; relative abundance: frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9514772-A1.  
 XX  
 PD 01-JUN-1995.  
 XX  
 PF 11-NOV-1994; 94WO-JP01916.  
 XX  
 PR 12-NOV-1993; 93JP-0355504.  
 XX  
 PA (MATS/) MATSUBARA K.  
 PA (OKUBO/) OKUBO K.  
 PI Matsubara K., Okubo K.  
 XX  
 DR WPI; 1995-206931/27.  
 XX  
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 XX  
 PS Claim 1; Page 1335; 2245pp; Japanese.  
 XX  
 CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in AAT19001-126837 and which is able to hybridise to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 CC  
 XX  
 SQ Sequence 548 BP; 126 A; 134 C; 121 G; 139 T; 28 other;  
 Query Match 40.5%; Score 32.8; DB 16; Length 548;  
 Best Local Similarity 75.5%; Pred. No. 1.7;  
 Matches 40; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 Oy 1 gagctaccagctaacaaaagcttaataagagagagtggtgagagaaa 53  
 Db 289 gagctgcgcgcgtcaccaagagcttcacacagggagagtggttaagangagagaa 341  
 RESULT 5  
 AAQ92546  
 ID AAQ92546 standard; DNA; 4691 BP.  
 XX  
 AC AAQ92546;  
 XX  
 DT 11-MAR-1996 (first entry)  
 XX  
 DE pComb3 expression vector.  
 XX  
 KW pComb3; phagemid expression vector; bacteriophage; coat protein 3;  
 KW Gene III; filamentous phage; minor phage coat protein; cpIII; cp3;  
 KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;  
 KW combinatorial Fab library; cassette; pG/cp3; lacZ promoter/operator;  
 KW ribosome binding site; RBS; pelB leader; spacer; tether sequence;  
 KW M4; pMT4-3; antibody; ss; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9511317-A1.  
 XX  
 PD 27-APR-1995.  
 XX  
 PF 19-OCT-1994; 94WO-US11907.  
 XX  
 PR 19-SEP-1994; 94US-0308841.  
 PR 19-OCT-1993; 93US-0139409.  
 PR 26-APR-1994; 94US-0233619.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 PA  
 PI Barbas CF, Burton DR, Lerner RA;  
 PI  
 DR WPI; 1995-170235/22.  
 XX  
 PT Synthetic human neutralising monoclonal antibodies to human  
 PT immunodeficiency virus - used for diagnosis and immuno:therapy of  
 PT HIV-induced disease  
 XX  
 PS Example 1; Page 185-188; 249pp; English.



DR	P-PSDB; AAY56286; AAY56287.
XX	
PT	New virus-like particle or gene delivery vehicle, useful for gene therapy -
XX	
PS	Claim 13; Fig 16; 66pp; English.
XX	
CC	The present invention describes a virus-like particle or gene delivery vehicle comprising a ligand capable of binding to a human amino acid transporter. The method is useful for the target delivery of substances to cells e.g. gene therapy. A human cationic amino acid transporter (hcART) targeted adenovirus is useful for local applications of adenoviral vector e.g. in patients with restenosis following balloon angioplasty where smooth muscle cells need to be transduced with an adenoviral vector carrying the CenOS cDNA. More efficient transduction of tissues can be carried out therefore resulting in lower multiplicity's of infections that can be used and therefore less vector associated toxicity to the tissues surrounding the target cells. AAZ38737 CC CC AAZ38770, and AAY56264 to AAY56287 represent sequences used in the exemplification of the present invention.
CC	
XX	
SQ	Sequence 5925 BP; 1454 A; 1487 C; 1517 G; 1467 T; 0 other;
Query Match	39.5%; Score 32; DB 21; Length 5925;
Best Local Similarity	79.2%; Pred. NO. 3.7;
Matches 38; Conservative	0; Mismatches 10; Indels 0; Gaps 0;
OY	1 gagccaccagtaacaaaagcttaataatagaaggagtgtaggagg 48  Db 2937 gacttcaccggtgacaagaagcctcaacagggaaggagtataaagg 2984
RESULT 8	
AAO92547	
ID	AAO92547 standard; DNA; 6166 BP.
AC	
XX	AAO92547;
XX	
DT	11-MAR-1996 (first entry)
XX	
DE	Expression vector, pho-TT.
XX	
KM	Human; Fcb; variable chain; heavy; light; region; VH; VL; HIV; gp120; 3b1; 3b3; 3b4; 3b9; M74; humanised; monoclonal antibody; Mab; immunoreaction; neutralisation; passive immunotherapy; tetanus toxin; alkaline phosphatase; phoa; ss; cyclic.
XX	
OS	Synthetic.
XX	
PN	WO9511317-A1.
PD	27-APR-1995.
XX	
PE	19-OCT-1994; 94WO-US11907.
XX	
PR	19-SEP-1994; 94US-0308841.
XX	
PR	19-OCT-1993; 93US-0139409.
XX	
PR	26-APR-1994; 94US-0233619.
XX	
PA	(SCRI ) SCRIPPS RES INST.
XX	
PI	Barbas CF, Burton DR, Lerner RA;
XX	
DR	WPI; 1995-170235/22.
XX	
PT	Synthetic human neutralising monoclonal antibodies to human immunodeficiency virus - used for diagnosis and immuno-therapy of HIV-induced disease
XX	
XX	Example 2; Page 193-197; 249pp; English.
CC	This sequence represents the expression vector, pPho-TT which is a

CC	modified version of the plasmid expression vector, pComb3 given in
CC	AA092546. phoA-TT provides for the expression of soluble fabs which are
CC	secreted into the periplasmic space which is regulated from the alkaline
CC	phosphatase (phoA) promoter. This plasmid was used within the scope of
CC	the invention to express various mutagenised human Fab's which comprise
CC	heavy and light variable regions which bind to HIV gp120. phoA-TT
CC	consists of a DNA molecule having two cassettes to express two soluble
CC	proteins a heavy chain and a light chain. The vector comprises,
CC	operatively linked 5' to 3', a first cassette consisting of the phoA
CC	promoter/operator sequences, an EcoRI restriction site, a ribosome
CC	binding site (RBS), an OmpA leader, a SfiI restriction site, a spacer
CC	region, a cloning region bordered by 5' sacI and 3' XbaI restriction
CC	sites, an NcoI restriction site between the two cassettes, and a second
CC	cassette consisting of an expression control RBS, a pelB leader, a human
CC	consensus amino terminus spacer region comprising the sequence EVQLLE,
CC	a cloning region bordered by 5' XhoI and 3' SpeI restriction sites
CC	followed by a SfiI site, expression control stop sequences and a NotI
CC	restriction site. The phoA-TT expression vector contains a light
CC	chain stuffer that is 1200 bp in length and a heavy chain stuffer that
CC	is 300 bp in length. The nucleotide sequences of the heavy and light
CC	chain stuffers encode the heavy and light chain variable domains of a
CC	tetanus toxin-specific Fab.
XX	
SQ	Sequence 6166 BP; 1416 A; 1706 C; 1629 G; 1415 T; 0 other;
Query Match	39.5%; Score 32; DB 16; Length 6166;
Best Local Similarity	62.5%; Pred. No. 3.8;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;	
QY	1 gagctaccagtaacaaaagcctaataagaggagtgttgaaggagaataatga 60
Db	
Db	5203 gacttcgcccgcacaaagcctcaacaaggggagtgtaattctagataatta 5262
OY	61 agaaacgctcatagcaatt 80
Db	
Db	5263 ggagggaatttaaatgaat 5282
RESULT	9
AAT61240	
ID	AAT61240 standard; DNA: 705 BP.
XX	
AC	AAT61240;
XX	
DT	13-MAY-1997 (first entry)
XX	
DE	Human anti-RSV monoclonal antibody RF-1 light chain DNA.
XX	
KM	Monoclonal antibody; Mab; RF-1; RF-2; respiratory syncytial virus;
KW	RSV; fusion protein; F-protein; Vaccine; immunotherapy; therapy;
KW	Epstein Barr virus; immortalisation; recombinant antibody; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	sig_peptide 1..60
FT	mat_peptide 61..702
FT	/*tag= a
FT	/*tag= b
XX	
PX	MO9640252-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US10070.
XX	
PR	07-JUN-1995; 95US-0488376.
XX	
PA	(IDEC-) IDEC PHARM CORP.
XI	Brams P, Chamat SS, Heard CJ, Newman RA, Pan L,
I1	Walsh EE;

XX WPI: 1997-099892/09.  
DR P-PSDB: AAM11638.  
XX  
XX Human monoclonal antibody specific for respiratory syncytial virus  
PT fusion protein - used for the prevention and treatment of RSV  
PT Infection  
XX  
XX Claim 9; Fig 9a; 85pp; English.  
XX  
XX A DNA sequence (AAT61240) codes for a polypeptide (AAM11638) comprising  
CC a leader sequence, RFL light chain variable region (see also  
CC AAM11634), and human kappa constant region. RFL is a human  
CC monoclonal antibody (hMab) specific for the fusion protein of  
CC respiratory syncytial virus (RSV). The DNA sequence, in vector  
CC NEOSPLA, can be used to produce the light chain construct in  
CC transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy  
CC and light chain constructs (see also AAT61241-42, AAT61279) are  
CC similarly used. The transfected host cells provide a constant,  
CC stable supply of anti-RSV F-protein hMabs for use in the treatment  
CC or prevention of RSV infection.  
XX  
SQ Sequence 705 BP; 178 A; 199 C; 177 G; 151 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 705;  
Best Local Similarity 83.7%; Pred. No. 3.3;  
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagcttaataagagagagtgtga 43  
||||| 11 11 ||||| 1111 11 11 ||||| 111111  
Db 663 gagctgcgcgcgtcacacaagagcttcacacagggagagtgtga 705

## RESULT 10

AAT61242  
ID AAT61242 standard; DNA: 708 BP.

AC AAT61242;

DT 13-MAY-1997 (first entry)

XX Human anti-RSV monoclonal antibody RF-2 light chain DNA.

DE Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;

KW RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;

KW Epstein Barr virus; immortalisation; recombinant antibody; ss.

KW Homo sapiens.

OS

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XX

XX

XX

PT fusion protein - used for the prevention and treatment of RSV  
PT Infection  
XX  
XX Claim 9; Fig 11a; 85pp; English.  
XX  
XX A DNA sequence (AAT61242) codes for a polypeptide (AAM11640) comprising  
CC a leader sequence, RF2 light chain variable region (see also  
CC AAM11636), and human kappa constant region. RF2 is a human  
CC monoclonal antibody (hMab) specific for the fusion protein of  
CC respiratory syncytial virus (RSV). The DNA sequence, in vector  
CC NEOSPLA, can be used to produce the light chain construct in  
CC transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy  
CC and light chain constructs (see also AAT61240-41, AAT61279) are  
CC similarly used. The transfected host cells provide a constant,  
CC stable supply of anti-RSV F-protein hMabs for use in the treatment  
CC or prevention of RSV infection.  
XX  
SQ Sequence 708 BP; 182 A; 196 C; 175 G; 155 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 708;  
Best Local Similarity 83.7%; Pred. No. 3.3;  
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagcttaataagagagagtgtga 43  
||||| 11 11 ||||| 1111 11 11 ||||| 111111  
Db 666 gagctgcgcgcgtcacacaagagcttcacacagggagagtgtga 708

## RESULT 11

AAA63530  
ID AAA63530 standard; DNA: 708 BP.

AC AAA63530;

DT 14-NOV-2000 (first entry)

XX DNA encoding a dimeric anti-CD20 light chain polypeptide.

DE

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PT misc\_feature 385..708  
FT /tag= d  
FT /note= "encodes human kappa light chain constant region"  
XX  
XX WO200044788-A1.  
XX  
XX 03-AUG-2000.  
XX  
XX 28-JAN-2000; 2000WO-US01893.  
XX  
XX 28-JAN-1999; 99US-0238741.

XX (IDEC-) IDEC PHARM CORP.  
 XX  
 PA  
 PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;  
 XX  
 DR WPI: 2000-514811/46.  
 DR P-PSDB: AAB08025.  
 XX  
 PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the  
 treatment of cancers, allergic disorders and autoimmune conditions -  
 XX  
 PS Example 1; Fig 1A-B; 65pp; English.  
 XX  
 PS The present sequence encodes a dimeric anti-CD20 light chain  
 CC polypeptide. The dimeric immunoglobulin is used in the method of the  
 CC invention. The specification describes a method for producing an  
 CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically  
 CC engineering a monoclonal antibody to introduce a cysteine molecule  
 CC which inhibits formation of intramolecular disulphide bridges between  
 CC sister heavy chains on the same antibody molecule. The dimer is a  
 CC homodimer or heterodimer that is capable of activating components of the  
 CC complement system, and has the ability to activate and kill cells via the  
 CC complement cascade. The dimer is also capable of binding to Fc gamma  
 CC receptors on cytotoxic effector cells and on host immune cells, and is  
 CC capable of initiating programmed cell death. The IgG/IgG dimers may be  
 CC used to treat allergic disorders, cancers and autoimmune diseases such  
 CC as allergic asthma, allergic bronchopulmonary aspergillosis, allergic  
 CC rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food  
 CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell  
 CC lymphomas. They may also be used to treat a range of other diseases and  
 CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,  
 CC pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes  
 CC mellitus, candidiasis and aplastic anaemia. They are also useful for  
 CC inducing hyper-cross-linking of membrane antigens and for the  
 CC preferential killing of selected cell populations.  
 XX  
 SQ Sequence 708 BP; 180 A; 196 C; 178 G; 154 T; 0 other;

Query Match 39.3%; Score 31.8; DB 21; Length 708;  
 Best Local Similarity 83.7%; Pred. No. 3.3;  
 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcacgtaacaaagcttaataagagagagtgtga 43  
 ||||| || || ||||| ||||| || || ||||| |||||  
 Db 666 gagctgcgcgtcacaaagagcttcaacagggagagtgtga 708

RESULT 12  
 AAT62511  
 ID AAT62511 standard; DNA: 720 BP.  
 XX  
 AC AAT62511;  
 XX  
 DT 25-MAY-1997 (first entry)  
 XX  
 DE Primatised anti-human B7.1 Antigen antibody 7B6 light chain DNA.  
 XX  
 KW Monoclonal antibody; cynomolgus monkey; macaque; 7B6;  
 KW primatised antibody; B7 antigen; CD28; immunosuppressive;  
 KW autoimmune disease; idiopathic thrombocytopenia purpura;  
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;  
 KW type 1 diabetes mellitus; graft versus host disease;  
 KW hetero-hybridoma; transectoma; ss.  
 XX  
 XX Chimeric Macaca cynomolgus;  
 OS Chimeric Homo sapiens.  
 XX  
 PN W09640878-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US10053.

XX 07-JUN-1995; 95US-0487550.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 XX  
 PI Anderson DR, Brams P, Hanna N, Shetlowsky WS;  
 XX  
 DR WPI: 1997-108638/10.  
 DR P-PSDB: AAW01819.  
 XX  
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen  
 PT useful for treating autoimmune disease or graft-versus-host disease  
 XX  
 PS Claim 9; Fig 9A; 81pp; English.  
 XX  
 PS 2 DNA sequences (AAT62511 and AAT13847) respectively code for  
 CC primatised forms (AAW01819 and AAW01820) of the light and heavy chains  
 CC of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody  
 CC 7B6. Cloned 7B6 light and heavy variable genes are inserted into  
 CC an expression vector (pref. NEO5PLA) which contains human light and  
 CC heavy chain constant region genes to allow prodn. of primatised  
 CC antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1  
 CC antibodies have also been produced (see also AAW01817-18 and AAW01821-  
 CC 22). The primatised antibodies inhibit the B7:CD28 pathway, making  
 CC them useful immunosuppressants for the treatment of autoimmune  
 CC disorders and graft-versus-host disease.  
 XX  
 SQ Sequence 720 BP; 178 A; 201 C; 192 G; 149 T; 0 other;

Query Match 39.3%; Score 31.8; DB 18; Length 720;  
 Best Local Similarity 83.7%; Pred. No. 3.3;  
 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 gagctcacgtaacaaagcttaataagagagagtgtga 43  
 ||||| || || ||||| ||||| || || ||||| |||||  
 Db 678 gagctgcgcgtcacaaagagcttcaacagggagagtgtga 720

RESULT 13  
 AAV35486  
 ID AAV35486 standard; DNA: 720 BP.  
 XX  
 AC AAV35486;  
 XX  
 DT 29-SEP-1998 (first entry)  
 XX  
 DE Macaque primatised 7B6 light chain DNA.  
 XX  
 KW Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;  
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;  
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;  
 KW immunogen; anti-idiotype reagent; Interleukin-2; IgG; immunoglobulin G;  
 KW T cell proliferation; ss.  
 XX  
 OS Macaca fascicularis.  
 XX  
 FH Key  
 FH CDS 1..720 Location/Qualifiers  
 FT /\*tag= a  
 FT /product= 7B6 light chain  
 XX  
 PN W09819706-A1.  
 PD 14-MAY-1998.  
 XX  
 PF 29-OCT-1997; 97WO-US19906.  
 XX  
 PR 08-NOV-1996; 96US-0746361.  
 XX  
 PA (IDEC-) IDEC PHARM CORP.  
 PA  
 PI Anderson DR, Brams P, Hanna N;

```
XX WP: 1998-286601/25.
DR P-PSDB: AAM63762.
XX
XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
PT inhibiting binding to CD28 - useful as specific immunosuppressants
PT for treating diseases that involve interactions between T and B
PT cells, e.g. graft rejection or tumours
XX
XX Example 7; Fig 4a; 87pp; English.
XX
XX This sequence encodes a primatized form of the antibody 7B6 light chain
CC from macaque. This sequence is used in a method which studies new
CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
CC Mab's are specific immunosuppressants for treatment of diseases involving
CC T cell/B cell interactions, particularly autoimmune disease, specifically
CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
CC host diseases, B cell lymphoma, infections (including by human immune
CC deficiency virus) or inflammatory disease and tumours. Optionally the
CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
CC also be used as imaging agents and as vaccines or immunogens to develop
CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
CC production of interleukin-2 (IL-2), T cell proliferation and
CC antigen-specific immunoglobulin G (IgG) responses.
XX
XX Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other:
SO
```

```
Query Match          39.3%; Score 31.8; DB 19; Length 720;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
Oy 1 gagctcaccagtaacaaaagcttaataagagagaggttga 43
    |||||  ||  |||||  |||||  ||  ||  |||||  |||||
Db 678 gagctgcgccgtcacacaagagcttcacagggagagagtgta 720
```

## RESULT 14

AA222287 standard; DNA; 725 BP.

AA222287;

20-DEC-1999 (first entry)

Nucleotide sequence of coding region of plasmid pSSpcyHuk.

Multimeric protein; immunoglobulin; receptor-ligand complex;  
hetero-dimeric receptor; trimeric G protein; transgenic; ss.

Synthetic.

W09949024-A2.

30-SEP-1999.

24-MAR-1999; 99WO-US06506.

25-MAR-1998; 98US-0079249.

(PLAN-) PLANET BIOTECHNOLOGY INC.

Wycoff KL, Jaiswal SK;

WPI: 1999-580446/49.

P-PSDB; AAY34096.

Producing heterologous multimeric proteins in plants, transformed with

```
PT several plasmids expressing polypeptide components, particularly for
PT immunoglobulins
XX
XX Example 1; Fig 5; 42pp; English.
XX
```

```
CC The invention relates to a method for producing heterologous, multimeric
CC proteins in plant cells. The method comprises: (a) transforming the cells
CC with several naked plasmids each encoding some, but not all, of the
CC polypeptide components of the multimeric proteins, and together providing
CC all the polypeptide components; and (b) culturing the cells. The method
CC is used to produce biologically active multimeric proteins particularly
CC immunoglobulins, receptor-ligand complexes, homo- or hetero-dimeric
CC receptors, or trimeric G proteins. This method provides properly
CC associated and assembled multimeric proteins in a fast and efficient
CC process, without the need to cross plants expressing single component of
CC the protein. Transgenic plants containing adjacent and stably integrated
CC plasmids, and their progeny can also express the multimeric proteins. The
CC present sequence represents the nucleotide sequence of the coding region
CC of the plasmid pSSpcyHuk. This plasmid contains a sequence encoding a
CC bean legumin signal peptide and a mouse light chain variable/human kappa
CC constant hybrid with linker sequences.
XX
```

Sequence 725 BP; 186 A; 199 C; 169 G; 171 T; 0 other:

```
Query Match          39.3%; Score 31.8; DB 20; Length 725;
Best Local Similarity 83.7%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Oy 1 gagctcaccagtaacaaaagcttaataagagagaggttga 43
    |||||  ||  |||||  |||||  ||  ||  |||||  |||||
Db 679 gagctgcgccgtcacacaagagcttcacagggagagagtgta 721
```

## RESULT 15

AAF30339 standard; CDNA; 6709 BP.

AAF30339;

14-MAY-2001 (first entry)

Bicistronic plasmid VR1605.

Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;  
immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1605;  
antibody; idiotype; vector; ss.

Chimeric - Cytomegalovirus.

Chimeric - Homo sapiens.

Chimeric - Bos taurus.

W0200109303-A2.

08-FEB-2001.

31-JUL-2000; 2000WO-US20679.

30-JUL-1999; 99US-0146170.

(VICA-) VICAL INC.

Hermanson GG;

WPI: 2001-123319/13.

Immunogenic compositions comprising Flt-3 ligand encoding  
polynucleotide and one or more antigen, or cytokine encoding  
polynucleotides, useful for suppressing tumour growth and for treating  
autoimmune diseases (e.g. rheumatoid arthritis) -

Example 1; Page 97-101; 149pp; English.

CC The present sequence is that of bicistronic plasmid VR1605, which  
 CC includes the cytomegalovirus immediate-early promoter, enhancer  
 CC and 5' untranslated sequences, human immunoglobulin kappa light  
 CC and gamma 1 heavy chain constant region DNA (pNegative) coding  
 CC sequences, and the transcriptional terminator region polyA and  
 CC termination signals from the bovine growth hormone gene. The  
 CC vector encodes no immunoglobulin variable regions, and therefore  
 CC does not express a functional protein. It serves as a negative  
 CC control for vaccination studies involving VR1623 (see AAF1623),  
 CC a bicistronic chimeric idiotype vector. Co-administration of  
 CC VR1623 with plasmid VR6200 (see AAF30313) encoding a secreted form  
 CC (see AAB20187) of mouse Fms-like tyrosine kinase (Flt-3 ligand),  
 CC demonstrated the ability of the present invention to enhance  
 CC protection from tumour challenge in a mouse B-cell lymphoma model.  
 XX

SQ Sequence 6709 BP; 1675 A; 1798 C; 1660 G; 1576 T; 0 other;

Query Match 39.3%; Score 31.8; DB 22; Length 6709;

Best Local Similarity 83.7%; Pred. No. 4.3; Mismatches 0; Gaps 0;

Matches 36; Conservative 0; Indels 7; Gaps 0;

Oy 1 gagctaccagtaacaaagcttaataagagagagtggtga 43

Db 2158 gagctgcgccgtacacaagaagcttaacacagagagagtggtga 2200

Search completed: January 5, 2002, 12:49:59  
 Job time: 4318 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:45:54 ; Search time 111.65 Seconds  
(without alignments)  
164.306 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 81

Sequence: 1 gagctcaccagtaacaaaaa.....gaaactgtctatagcatly 81

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	4691	4	US-08-591-632-43
2	32	39.5	6166	4	US-08-591-632-51
3	31.8	39.3	705	1	US-08-488-376-16
4	31.8	39.3	705	2	US-08-634-223-16
5	31.8	39.3	705	2	US-08-634-224-16
6	31.8	39.3	705	2	US-08-634-400-16
7	31.8	39.3	705	2	US-08-635-878-16
8	31.8	39.3	705	2	US-08-770-057-16
9	31.8	39.3	705	4	US-09-335-697B-16
10	31.8	39.3	708	1	US-08-488-376-18
11	31.8	39.3	708	2	US-08-634-223-18
12	31.8	39.3	708	2	US-08-634-224-18
13	31.8	39.3	708	2	US-08-634-400-18
14	31.8	39.3	708	2	US-08-635-878-18
15	31.8	39.3	708	2	US-08-770-057-18
16	31.8	39.3	708	4	US-09-335-697B-18
17	31.8	39.3	720	3	US-08-487-550-5
18	31.8	39.3	8540	1	US-08-149-099C-2
19	31.8	39.3	8540	2	US-08-478-967A-2
20	31.8	39.3	8541	1	US-08-478-967A-1
21	31.8	39.3	9209	1	US-08-149-099C-3
22	31.8	39.3	9209	2	US-08-476-275-2
23	31.8	39.3	9209	2	US-08-478-967A-3
24	31.8	39.3	18986	2	US-08-819-866-2
25	31.8	39.3	18986	2	US-09-023-715-2
26	31.4	38.8	117	3	US-08-284-516C-34
27	31.4	38.8	117	3	US-08-284-516C-35

28	31.4	38.8	3169	3	US-08-630-820-5	Sequence 5, Appl
29	31.2	38.5	780	3	US-09-027-449-54	Sequence 54, Appl
30	31.2	38.5	780	3	US-09-027-449-58	Sequence 58, Appl
31	31.2	38.5	780	3	US-09-027-449-65	Sequence 65, Appl
32	31.2	38.5	780	3	US-08-804-444A-54	Sequence 54, Appl
33	31.2	38.5	780	3	US-08-804-444A-58	Sequence 58, Appl
34	31.2	38.5	780	3	US-09-026-985-54	Sequence 54, Appl
35	31.2	38.5	780	3	US-09-026-985-58	Sequence 58, Appl
36	31.2	38.5	780	3	US-09-026-985-65	Sequence 65, Appl
37	31.2	38.5	2143	3	US-09-097-309-5	Sequence 9, Appl
38	31.2	38.5	2143	4	US-09-097-171A-9	Sequence 9, Appl
39	31.2	38.5	2178	1	US-08-463-587A-24	Sequence 24, Appl
40	31.2	38.5	2178	2	US-08-463-667A-2	Sequence 2, Appl
41	31.2	38.5	2178	3	US-08-923-854-24	Sequence 24, Appl
42	31.2	38.5	2178	5	PCT-US91-09133-25	Sequence 25, Appl
43	31.2	38.5	6127	2	US-08-887-352B-1	Sequence 1, Appl
44	31.2	38.5	6127	4	US-09-109-207C-1	Sequence 1, Appl
45	31.2	38.5	6127	4	US-09-296-005-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-591-632-43  
Sequence 43, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbados, Carlos F.  
APPLICANT: Burton, Dennis R.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESS: Patent Counsel  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2837  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4691 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-591-632-43

Query Match 39.5%; Score 32; DB 4; Length 4691;  
Best Local Similarity 62.5%; Pred. No. 0.73;  
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagctttaataagagagagtggtgaggaagaaaaaaatga 60  
DB 3273 GAGTTCGCCCGTCACAAAGAGCTTCACAGAGGAGAGTGTTATTCTAGATTAAATTA 3332

OY 61 agaaacgtctataagcaatt 80  
DB 3333 GGAGGAATTTAAATGAAT 3352

RESULT 2  
US-08-591-632-51  
Sequence 51, Application US/08591632  
Patent No. 6261558  
GENERAL INFORMATION:  
APPLICANT: Barbas, Carlos F.  
APPLICANT: Burton, Dennis R.  
APPLICANT: Lerner, Richard A.  
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591.632  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/11907  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,841  
FILING DATE: 19-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/233,619  
FILING DATE: 26-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,409  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: JSRI 332.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937  
TELEFAX: (619) 784-9399  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-591-632-51

Query Match 39.5%; Score 32; DB 4; Length 6166;  
Best Local Similarity 62.5%; Pred. No. 0.76;  
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 1 gagctcaccagtaacaaaagctttaataagagagagtggtgaggaagaaaaaaatga 60  
DB 5203 GAGTTCGCCCGTCACAAAGAGCTTCACAGAGGAGAGTGTTATTCTAGATTAAATTA 5262

OY 61 agaaacgtctataagcaatt 80  
DB 5263 GGAGGAATTTAAATGAAT 5282

RESULT 3  
US-08-488-376-16  
Sequence 16, Application US/08488376  
Patent No. 5811524  
GENERAL INFORMATION:  
APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Soulaïma Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
APPLICANT: NEWMAN, Roland Anthony  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,376  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 705 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..705  
US-08-488-376-16

Query Match 39.3%; Score 31.8; DB 1; Length 705;  
Best Local Similarity 83.7%; Pred. No. 0.65;  
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 663 GAGTTCGCCCGTCACAAAGAGCTTCACAGAGGAGAGTGTTGA 705

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RESULT 4
US-08-634-223-16
: Sequence 16, Application US/08634223
: Patent No. 5840298
: GENERAL INFORMATION:
: APPLICANT: BRAMS, Peter
: APPLICANT: CHAMAT, Soulaïma Salim
: APPLICANT: PAN, Li-Zhen
: APPLICANT: WALSH, Edward E.
: APPLICANT: HEARD, Cheryl Janne
: APPLICANT: NEWMAN, Roland Anthony
: TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
: TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/634,223
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/488,376
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-150
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
: US-08-634-223-16

Query Match 39.3%; Score 31.8; DB 2; Length 705;
Best Local Similarity 83.7%; Pred. No. 0.65;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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||||| | | | | | | | | | | | | | | | | | | | |
Db 663 GAGCTGCCCGCTCAACAAGAGCTTCAACAGGAGAGAGTGTGCA 705

RESULT 5
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: Sequence 16, Application US/08634224
: Patent No. 5866125
: GENERAL INFORMATION:
: APPLICANT: BRAMS, Peter
: APPLICANT: CHAMAT, Soulaïma Salim
: APPLICANT: PAN, Li-Zhen

```

```

1 APPLICANT: WALSH, Edward E.
2 APPLICANT: HEARD, Cheryl Janne
3 APPLICANT: NEWMAN, Roland Anthony
4 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
5 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
6 TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
7 NUMBER OF SEQUENCES: 19
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Burns, Doane, Swecker & Mathis
10 STREET: P.O. Box 1404
11 CITY: Alexandria
12 STATE: Virginia
13 COUNTRY: United States
14 ZIP: 22313-1404
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentln Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/634,224
21 FILING DATE:
22 CLASSIFICATION: 424
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/488,376
25 FILING DATE: 07-JUN-1995
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Teskin, Robin L.
28 REGISTRATION NUMBER: 35,030
29 REFERENCE/DOCKET NUMBER: 012712-150
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (703) 836-6620
32 TELEFAX: (703) 836-2021
33 INFORMATION FOR SEQ ID NO: 16:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 705 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: DNA (genomic)
40 FEATURE:
41 NAME/KEY: CDS
42 LOCATION: 1..705
43 US-08-634-224-16
44
45 Query Match 39.3%; Score 31.8; DB 2; Length 705;
46 Best Local Similarity 83.7%; Pred. No. 0.65;
47 Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
48
49 OY 1 gagctaccaglaacaaaagcttaataagagagagtgtga 43
50 ||||||| 11 ||||||| 11111 11 ||||||| 11111
51 Db 663 GAGCTCGCCCGCTCACAAAGAGCTTCAACAGGAGGAGACTGTGGA 705
52
53 RESULT 6
54 US-08-634-400-16
55 Sequence 16, Application US/08634400
56 Patent No. 5939068
57 GENERAL INFORMATION:
58 APPLICANT: BRAMS, Peter
59 APPLICANT: CHAMAT, Soulaïma Salim
60 APPLICANT: PAN, Li-zhen
61 APPLICANT: WALSH, Edward E.
62 APPLICANT: HEARD, Cheryl Janne
63 APPLICANT: NEWMAN, Roland Anthony
64 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
65 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
66 TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
67 NUMBER OF SEQUENCES: 19
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Burns, Doane, Swecker & Mathis
70 STREET: P.O. Box 1404

```

```

CITY : Alexandria
STATE : Virginia
COUNTRY : United States
ZIP : 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER : IBM PC compatible
OPERATING SYSTEM : PC-DOS/MS-DOS
SOFTWARE : PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,400

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376

FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME : Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127212-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
US-08-634-400-16

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Query Match      39.3%; Score 31.8; DB 2; Length 705;
Best Local Similarity 83.7%; Pred. No. 0.65;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 gacgcacccagtlacaaaagccttaataagagagagatgtga 43
        ||||| | | | | | | | | | | | | | | | | | | | |
Db      663 GAGCTCGCGCGCTCACAAAGAGCTTCACACAGCGGAGACTGTGA 705

RESULT 7
US-08-635-078-16
: Sequence 16, Application US/08635878
: Patent No. 5955364
GENERAL INFORMATION:
APPLICANT: BRAWS, Peter A.
APPLICANT: CHAMAT, Souleima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEURALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/08/635,878
2 FILING DATE:
3 CLASSIFICATION:
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 08/488,376
6 FILING DATE: 07-JUN-1995
7 ATTORNEY/AGENT INFORMATION:
8 NAME: Teskil, Robin L.
9 REGISTRATION NUMBER: 35,030
10 REFERENCE/DOCKET NUMBER: 012712-150
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (703) 836-6620
13 TELEFAX: (703) 836-2021
14 INFORMATION FOR SEQ ID NO: 16:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 705 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: DNA (genomic)
21 FEATURE:
22 NAME/KEY: CDS
23 LOCATION: 1..705
24 US-08-635-878-16

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	Query Match	Score 31.8;	DB 2.	Length 705;
	Best Local Similarity	Pred. No. 0.65;		
	Matches	Conservative 36;	Mismatches 7;	Gaps 0.
Qy	1 gagctaccacgataacaagaaggcttaactatagaaagaagtgttga	43		
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RESULT 8  
 US-08-770-057-16  
 Sequence 16, Application US/08770057  
 Patent No. 5958765  
 GENERAL INFORMATION:  
 APPLICANT: BRAMS, Peter  
 APPLICANT: CHAMAT, Soulaïma Salim  
 APPLICANT: PAN, Li-zhen  
 APPLICANT: WALSH, Edward E.  
 APPLICANT: HEARD, Cheryl Janne  
 APPLICANT: NEWMAN, Roland Anthony  
 TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F'-PROTEIN AND  
 TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Burns, Doane, Swecker & Mathis  
 STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/770,057  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/488,376  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 REFERENCE/DOCKET NUMBER: 012712-150





	Query Match	39.3%	Score 31.8;	DB 2.	length 708;
	Best Local Similarity	83.7%;	Pred. No. 0.65;		
	Matches	36;	Conservative	0;	Mismatches 7; Indels 0;
Oy	1	gagctaccagtaacaaaagcgttaataatagagagagtgttga	43		
Db	666	GAGCTCGCCCGTCACAAAGAGCCTTCAAACGAGGGGAAGAGCTTTGA	708		

```

QY      1  gagctcaccagtaacaaaaagcttaatatagagagagtglttga 43
          |||||  |||  |||||  |||||  |||  |||  |||||  |||||
Db      666  GAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTGA 708

```

US-08-770-057-18  
 RESULT 15  
 Sequence 18, Application US/08770057  
 Patent No. 5958765  
 GENERAL INFORMATION:  
 APPLICANT: BRAMS, Peter  
 APPLICANT: CHAMAT, Soulatma Salim  
 APPLICANT: PAN, Li-zhen  
 APPLICANT: WALSH, Edward E.  
 APPLICANT: HEARD, Cheryl Janne  
 APPLICANT: NEWMAN, Roland Anthony  
 TITLE OF INVENTION: NEURALIZING HIGH AFFINITY HUMAN  
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
 TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Burns, Doane, Swecker & Mathis  
 STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/770,057  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/488,376  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030

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; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..708
; US-08-770-057-18

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Query Match          39.3%; Score 31.8; DB 2; Length 708;
Best Local Similarity 83.7%; Pred. No. 0.65;
Matches 36; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Search completed: January 5, 2002, 12:45:56  
 Job time: 4280 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 5, 2002, 12:15:52 ; Search time 2209.96 Seconds  
(without alignments)  
393.857 Million cell updates/sec

Title: US-09-875-221A-115

Perfect score: 81

Sequence: 1 gagctcaccagtaacacaaaa.....gaaactctatagcaatg 81

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
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20: em\_gss\_vrl:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	36.6	44.4	883	11	BG756095 602716589
6	35.6	44.0	313	10	AI815108 x
7	35.4	43.7	251	10	AM270172 x072c08.x
8	35.4	43.7	957	11	BG756233 602713544
9	34.4	42.5	302	11	BF834388 C02-HT096
10	34.4	42.5	367	11	BF174509 MEX3290a
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12	34.4	42.5	744	11	BG686771 602650742

13	34.4	42.5	753	11	BG756401	BG756401 602715727
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15	34.4	42.5	841	11	BG758779	BG758779 602713139
16	34.4	42.0	221	10	AM238200	AM238200 x02a06.x
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22	34.4	42.0	472	11	BF664009	BF664009 602145683
23	34.4	42.0	787	11	BG536224	BG536224 602565445
24	34.4	42.0	1100	11	BF663472	BF663472 602144635
25	33.8	41.7	750	11	BG755394	BG755394 602713951
26	33.8	41.7	864	11	BG686067	BG686067 602638637
27	33.4	41.2	291	10	AM512732	AM512732 x00612.x
28	33.4	41.2	484	10	AI538356	AI538356 tp64f03.x
29	33.4	41.2	496	10	AI864507	AI864507 wj93d04.x
30	33.4	41.2	776	11	BG684027	BG684027 602635634
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33	33.4	41.2	865	11	BG617325	BG617325 602615353
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35	33.2	41.0	733	11	BG483124	BG483124 602503060
36	33.2	41.0	905	11	BG754585	BG754585 602714527
37	33.2	41.0	988	11	BG756209	BG756209 602713519
38	33.2	40.7	215	10	AM793129	AM793129 CM4-QM000
39	32.8	40.5	190	10	AU165104	AU165104 AU165104
40	32.8	40.5	210	10	BE711101	BE711101 RC3-HT064
41	32.8	40.5	299	10	AA933587	AA933587 cm61h09.s
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#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
mRNA sequence.  
ACCESSION  
BG757770  
VERSION  
BG757770.1 GI:14068423  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rudin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCMT1703 row: d column: 22  
High quality sequence stop: 736.  
Location/Qualifiers

#### FEATURES

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/clone="IMAGE:4854885"  
/clone\_id="NIH\_MGC\_48"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"

*Note:* \*Organ: B-cells; Vector: pORF3; Site.1: XhoI; Site.2: EcoRI. cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). *Note:* this is a NIH-MGC Library.†

BASE COUNT	197	a	247	c	207	g	191	t
------------	-----	---	-----	---	-----	---	-----	---

	Query Match	45.2%	Score 36.6;	DB 11:	Length 842;
	Best Local Similarity	82.4%;	Pred.	No. 1,3e+02	
	Matches 42;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0;
OY	1 gaagctaccacgtaaacaaaagcgtttaataagaaggaagtgttcaaggagaa	51			
DG	688 GAGCGTGGCCCGTCACGAAGAAGCTTGTAACCGGGCAAGTAGGTACGAGGCATAA	738			

RESULT	2
A1683231/c	
LOCUS	560 bp mRNA
DEFINITION	tX02b10.x1 NCI CGAP hp4 Homo sapiens cDNA IMAGE:2267995 3' EST
	similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN)
	); mRNA sequence.
ACCESSION	A1683231
VERSION	A1683231.1 GI:4893403
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
1 (bases 1 to 560)  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.  
National Cancer Institute, Cancer genome Anatomy project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/URL at: [www-bio.linnl.gov/dbtrp/lmage/lmage.html](http://www-bio.linnl.gov/dbtrp/lmage/lmage.html)  
Insert Length: 1020 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality stop: 198.  
Location/Qualifiers

```

/db_xref="taxon:9606"
/clone="IMAGE:2267995"
/clone.lib="NCI CGAP v14"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: PCMV-SpOrt6; site_1: SalI;
site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
BASE COUNT      111 a      128 c      172 g      149 t
ORIGIN

```

Query Match	44.4%	Score 36;	DB 10;	Length 560;
Best Local Similarity	80.8%;	Pred. No. 2e+02;		
Matches 42;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;

OY 1 gactcaccagtaacaaaaagctttaatagaygaagtgtltgagygagaaaa 52  
||||| || | |||| ||||| | | ||||| ||||| |||||  
Db 279 GAGCTCGCCCGTCCCAAGAGAGCTTCACACAGGGGAGAGGTTTAAGGGGMAAA 228

RESULT	3
B6685433	
LOCUS	844 bp mRNA EST 01-MAY-2001
DEFINITION	60265728f1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4765292 5'
ACCESSION	B6685433
VERSION	B6685433
KEYWORDS	B6685433.1 GI:13916830
SOURCE	EST.
ORGANISM	human. Homo sapiens Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
Mammalia: Eutheria: Primates: Catarrhini: Homiinae: Homo-  
1 (bases 1 to 844)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 plate: LINC1623.row: 0 column: 21  
 High quality sequence: stop: 839.  
 High quality sequence: fdb:

```

Source
1. .844
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4765292"
/clone_1bp="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B cells; Vector: pORF7. Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT
195 a      261 c      212 g      176 t
ORIGIN

```

	Query Match	44.4%	Score 36	DB 11	Length 844
	Similarity	80.8%	Pred No. 1.7e+02		
	Best Local				
	Matches 42	Conservative 0	Mismatches 10	Indels 0	Gaps 0
OY	1 gacgtccaccagtaaacaaaagctttaataagayggagagtgttcgagaagaaaa	52			
Db	678 GAGCTGGCCGCGTCAACAAAGAGCTTTAACAAGGGGAAGAAGTGTATTAAGGGGCCAAH	729			

LOCUS	BC6885152	883 bp	mRNA	EST	01-MAY-2001
DEFINITION	602637032n1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764919 5',				
mRNA sequence.					
ACCESSION	BC6885152				
VERSION	BC6885152.1	GI:13916549			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 883)  
TITLE NIH-MGC http://mhc.nci.nih.gov/  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM1622 row: p column: 08  
High quality sequence stop: 838.

FEATURES  
source  
1. 883  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="NIH-MGC\_48"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
Site:2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(5). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library." 2 others

BASE COUNT 214 a 260 c 222 g 185 t  
ORIGIN

Query Match 44.4% Score 36; DB 11; Length 883;  
Best Local Similarity 80.8%; Pred. No. 1.7e+02;  
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 gacgtccagtgataaagcttaagagagagtggtgagaggaataa 52  
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 675 GACGTCCGCGTCACAAAGAGCTTCAACAGGAGAGTGTAGAGGGGGA 726

RESULT 5  
LOCUS BG756095 883 bp mRNA EST 15-MAY-2001  
DEFINITION 602716589F1 NIH-MGC\_48 Homo sapiens cDNA clone IMAGE:4856374 5',  
mRNA sequence.  
ACCESSION BG756095  
VERSION BG756095.1 GI:14066748  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 883)  
NIH-MGC http://mhc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM1707 row: b column: 23

FEATURES High quality sequence stop: 869.  
source  
1. 883  
Location/Qualifiers

1. 883  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:4856374"  
/tissue\_type="NIH-MGC\_48"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
Site:2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(5). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC Library."

BASE COUNT 217 a 252 c 219 g 195 t  
ORIGIN

Query Match 44.4% Score 36; DB 11; Length 883;  
Best Local Similarity 80.8%; Pred. No. 1.7e+02;  
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 gacgtccagtgataaagcttaagagagagtggtgagaggaataa 52  
||||| 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 665 GACGTCCGCGTCACAAAGAGCTTCAACAGGAGAGTGTAGAGGGGGA 716

RESULT 6  
LOCUS A1815108/c 313 bp mRNA EST 07-MAR-2000  
DEFINITION wR71b04.x1 NCI-CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2420815 3',  
similar to gb:m63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN  
); mRNA sequence.  
ACCESSION A1815108  
VERSION A1815108.1 GI:5426323  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS 1 (bases 1 to 313)  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert length: 929 Std Error: 0.00  
Seq primer: -400p from GIBCO.

FEATURES  
source  
1. 313  
Location/Qualifiers

1. 313  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="NCI-CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 71 a 62 c 93 g 87 t  
ORIGIN

	Query Match	44.0%	Score 35.6;	DB 10;	Length 313;
	Best Local Similarity	82.0%;	Pred. No. 3.1e+02;		
Matches	41; Conservative	0;	Mismatches	9;	Indels 0;
Oy	1 gagcaccacgaatacaaaaagcttaatatagaagaaagtgtttaagaa	50			
Dd	259 gagcttcgccccgacacaaaagcttcaaacaggagaaagtgttacgggcaca	210			

RESULT	7
AM270172	
LOCUS	AM270172 251 bp mRNA
DEFINITION	xp122cc08.x1 NCI_CGAP_O4 Homo sapiens CDNA clone IMAGE:2745902 3 similar to gb:S49006 IG KAPPA CHAIN C REGION (HUMAN); mRNA sequence.
ACCESSION	AM270172
VERSION	AM270172.1
KEYWORDS	EST.
SOURCE	human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 251)  
 NCJ-CGAP <http://www.ncbi.nlm.nih.gov/ncjgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 COMMENT

**JOURNAL COMMENT**  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [casabs-remail.nih.gov](mailto:casabs-remail.nih.gov)  
 Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,  
 Michael R. Emmert-Buck M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: Greg Lencov, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/MLND at:  
[www-bio.llnl.gov/bdnp/image/image.html](http://www-bio.llnl.gov/bdnp/image/image.html)

Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 250.

```
FEATURES      Location/Qualifiers
source        1 . .251 .
```

```

/organism="Homo-sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2745902"
/clone_lib="NCI_CGAP_Ov40"
/sex="Female"
/issue_type="endometrialid ovarian metastasis"
/lab_host="DH10B"
/notes="Organ: ovary; Vector: PAMP10; cDNA made by oligo-dt
priming; Non-directionally cloned into the UDG sites of
PAMP10. Size-selected on agarose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

```

Query Match	43.7%	Score 35.4	DB 10	Length 251
Best Local Similarity	76.4%	Pred. No. 3.6e+02		
Matches 42	Conservative 0	Mismatches 13	Indels 0	Gaps 0

**Oy**      1 gaactcaccagtaacaaaaagctttaataagaygaagtgltggyagyaaaaaaa 55  
         ||||| | | | | | | | | | | | | | | | | | | | |  
**D6**      55 GAGCTCGCCCGTCACAAGAGAGCTTCAACAGGAGGTGTTAGAGGGGAANAANNA 100

RESULT	8
BG756233	

LOCUS	BG756233	957 bp	mRNA	15-MAY-2001
DEFINITION	602713544F1 NIH_MGC_Homo sapiens cDNA clone IMAGE:4853795 5',			
ACCESSION	BG756233			
VERSION	BG756233.1			
KEYWORDS	EST.			
SOURCE	human.			

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 957)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L1CMT100 row: 9 column: 12  
 High quality sequence stop: 837.

FEATURES	Location/Qualifiers
source	1. .957

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4853795"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; site_1: XhoI;
site_2: EcoRI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH-MGC Library."

```

BASE COUNT	240 a	280 c	230 g	206 t	1 others
ORIGIN					
Query Match		43.7%	Score 35.4	DB 11	Length 957
Best Local Similarity		79.2%	Pred. No. 2.2e+02		
Matches 42: Conservative		0	Mismatches 11	Indels 0	Gaps 0

Oy 1 gagctcaccagtaacaaaaagctttaatagagagagagctttagagagaaaaa 53  
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 640 GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGGTGTAGAGGCAAGAAA 697

RESULT		9	
LOCUS	BF834386/c		
DEFINITION	BF834388	302 bp	mRNA EST
ACCESSION	CN2-HT0969-111100-513-g04	HT0969	Homo sapiens CDNA, mRNA sequence
VERSION	BF834388		
KEYWORDS	EST.		
SOURCE	human,		
ORGANISM	Homo sapiens		

REFERENCE  
AUTHORS  
1 (bases 1 to 302)  
Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M. R.,  
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,  
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,  
Brunstein, A. J., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare  
, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and  
Simpson, A. J.

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL MEDLINE COMMENT	<p>Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)</p> <p>Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br</p> <p>This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?vl=CM2&amp;t2=CM2-Hr0969-111100-513-g04&amp;f3=2000-11-11&amp;v4=1) Seq primer: puc18 forward High quality sequence start: 5. High quality sequence stop: 302.</p>					
FEATURES	Location/Qualifiers					
SOURCE	1..302 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="HR0969" /dex_stage="Adult"					
BASE COUNT	/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
ORIGIN	48 a                84 c                83 g                87 t					
Query Match	42.5%; Score 34.4; DB 11; Length 302;					
Best Local Similarity	78.8%; Pexp.No. 5.4e+02;					
Matches 41:	Conservative 0; Mismatches 11; Indels 0; Gaps 0;					
OY	1 gagccaccagtaacaaagaacttaatacaggaagatctttaggaggaaaa 52   Db      65 GAGCTCGCCGCGTCACAAAGACTTCAACAGGGGAGAGTGTTAGAGGGAGAGA 14					
RESULT 10						
BFI74509	EST                23-MAR-2001					
LOCUS	BFI74509                367 bp                mRNA					
DEFINITION	MYE3290a Myeloma (MTE) CDNA library Homo sapiens CDNA, mRNA sequence.					
ACCESSION	BFI74509					
VERSION	BFI74509.1 GI:13440723					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 367) Claudio J.O., Tang,H., Khan,E.M., Vorralla,M., Li,Z., Cukerman,E., Francisco-Pabalan,O., Liew,C.C. and Stewart,A.K.					
TITLE	The transcriptional phenotype of myeloma cells					
JOURNAL COMMENT	Unpublished (2000) Contact: A. Keith Stewart, M.D. Oncology Research University Health Network 610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada Tel: (416) 946-4639 Fax: (416) 946-6546 Email: k.stewart@utoronto.ca					
PCR PRIMERS	FORWARD: 5'-GCCAAGCTCGAATTAACCTCAAGG-3' BACKWARD: 5'-CAGAGTCATTGTATACGACTCACTATAGGCGC-3' Seq primer: 5'-GAATTTAACCTCATCAAGG-3'.					

FEATURES	Location/Qualifiers
Source	1. 367
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_id="Myeloma (MYE) CDNA library"
	/sex="male"
	/tissue-type="Blood"
	/cell-type="myeloma"
	/dev_stage="multiple myeloma"
	/note="Vector: Lambda Zap Express; site_1: EcoRI; site_2: XhoI; Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and a-32PldATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10 <sup>6</sup> . Clones from the primary library were randomly selected for single pass sequencing."
BASE COUNT	96 a 116 c 80 g 74 t 1 others
ORIGIN	
Query Match	42.5%; Score 34.4; DB 11; Length 367;
Best Local Similarity	78.8%; Pred. No. 5e+02;
Matches	41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Oy	1 gagctcaccagatatacaaaagcttaataagaggagagctgttgaggagaa 52
	11 11 11 11 11 11 11 11 11 11 11 11
Db	133 GAGCTCGCCCTCACAAAGAGCTTCACAGGAGAGTGTTAAGAGGAGAA 184
RESULT 11	
LOCUS	H25972 391 bp mRNA EST 10-JUL-1995
DEFINITION	y156d07.r1 Soares breast 3Nbstr Homo sapiens CDNA clone
	IMAGE:162253 5' similar to gp:S49006 IG KAPPA CHAIN C REGION (HUMAN
	); mRNA sequence.
ACCESSION	H25972
VERSION	H25972.1 GI:895095
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 391)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
	,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
	Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
	,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The WASHU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@watson.wustl.edu
	Insert Size: 664
	High quality sequence stops: 307
	Source: IMAGE Consortium, LNL
	This clone is available royalty-free through LNL; contact the
	IMAGE Consortium (info@image.lnl.gov) for further information.
	InsertLength: 664 Std Error: 0.00

FEATURES	Location/Qualifiers
Source	1. 367
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_id="Myeloma (MYE) CDNA library"
	/sex="male"
	/tissue-type="Blood"
	/cell-type="myeloma"
	/dev_stage="multiple myeloma"
	/note="Vector: Lambda Zap Express; site_1: EcoRI; site_2: XhoI; Myeloma cells from multiple myeloma patients' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MuV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and a-32PldATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10 <sup>6</sup> . Clones from the primary library were randomly selected for single pass sequencing."
BASE COUNT	96 a 116 c 80 g 74 t 1 others
ORIGIN	
Query Match	42.5%; Score 34.4; DB 11; Length 367;
Best Local Similarity	78.8%; Pred. No. 5e+02;
Matches 41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
Db 133	GAGCTCGCCCTCACAAAGAGCTTCACAGGAGGTGTAAAGAGGAGAA 184
Oy 1	gaagtcaccagtaacaaaagcttaataagaggagagtggtgagagagaaa 52
	11 11 11 11 11 11 11 11 11 11 11 11
RESULT 11	
LOCUS	H25972 391 bp mRNA EST 10-JUL-1995
DEFINITION	y156d07.r1 Soares breast 3Nbstr Homo sapiens CDNA clone
	IMAGE:162253 5' similar to gp:S49006 IG KAPPA CHAIN C REGION (HUMAN
	); mRNA sequence.
ACCESSION	H25972
VERSION	H25972.1 GI:895095
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 391)
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
	,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
	Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
	,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The WASHU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK
	Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
	Tel: 314 286 1800
	Fax: 314 286 1810
	Email: est@watson.wustl.edu
	Insert Size: 664
	High quality sequence stops: 307
	Source: IMAGE Consortium, LNL
	This clone is available royalty-free through LNL; contact the
	IMAGE Consortium (info@image.lnl.gov) for further information.
	InsertLength: 664 Std Error: 0.00



Db 663 GAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 714

RESULT 14  
LOCUS BG755364 782 bp mRNA EST 15-MAY-2001  
DEFINITION 602713920F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4854173 5',  
mRNA sequence.  
ACCESSION BG755364  
VERSION BG755364.1 GI:14066017  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished. (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLCMT701 row: 9 column: 06  
High quality sequence stop: 728.  
Location/Qualifiers  
1. 782  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:4854173"  
/clone\_lib="NIH\_MGC\_48"  
/issue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
Site: 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(5). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 194 a 231 c 201 g 156 t

ORIGIN

Query Match 42.5%; Score 34.4; DB 11; Length 782;  
Best Local Similarity 78.8%; Pred. No. 3.7e+02;  
Matches 41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 687 GAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 738

ORIGIN

RESULT 15  
LOCUS BG758779 841 bp mRNA EST 15-MAY-2001  
DEFINITION 602713139F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4853553 5',  
mRNA sequence.  
ACCESSION BG758779  
VERSION BG758779.1 GI:14069432  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 841)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished. (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLCMT699 row: m column: 10  
High quality sequence stop: 839.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/issue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
Site: 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(5). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 204 a 257 c 208 g 172 t

ORIGIN

Query Match 42.5%; Score 34.4; DB 11; Length 841;  
Best Local Similarity 78.8%; Pred. No. 3.6e+02;  
Matches 41; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 678 GAGCTCGCCGTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGGAGAAA 729

ORIGIN

Search completed: January 5, 2002, 12:15:55  
Job time: 5639 sec

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